

JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;

Genentech Inc. (US)

Location/Qualifiers

1. 11679

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 498 a 432 c 419 g 330 t

ORIGIN

Query Match 100.0%; Score 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX454470 1679 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 55' from Patent WO0208284.
ACCESSION AX454470
VERSION AX454470.1 GI:21713859
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 55 31-JAN-2002;

Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L., and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same

JOURNAL Patent: WO 0140466-A 375 07-JUN-2001;

Genentech Inc. (US)

FEATURES Location/Qualifiers

1..1679 /organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 498 a 432 c 419 g 330 t

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Query Match 100.0% Score 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
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RESULT 6

AX490948

LOCUS

DEFINITION

AX490948

VERSION

AX490948.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

AX490948 1679 bp DNA linear PAT 16-AUG-2002
Sequence 55 from Patent WO0200690.

AX490948

AX490948.1

GI:22323811

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Baker, K. P., Ferrara, N., Gerber, H., Gerritsen, M. E., Goddard, A.,

Godowski, P. J., Gurney, A. L., Hillen, K. J., Masters, S. A., Pan, J.,

Paoletti, N. F., Stephan, J. P., Watanabe, C. K., Williams, P. M., Wood, W. L.

and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0200690-A 55 03-JAN-2002;
Genentech, Inc. (US)
Location/Qualifiers
1. 1679
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 498 a 432 c 419 g 330 t.
ORIGIN
Query Match 100.0%; Score: 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGTGCTCTTACGAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGACCAAC 60
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LOCUS AX665342 1839 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 100 from Patent WO03002765.
ACCESSION AX665342
VERSION AX665342.1 GT:29290464
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS Sellar, G.C. and Gabra, H.
TITLE Cancer: WO 03002765-A 100 09-JAN-2003;
JOURNAL Patent: WO 03002765-A 100 09-JAN-2003;
Cancer Research Technology Limited (GB)

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Query Match	85.3%	Score 1432.8	DB 9	Length 1839
Best Local Similarity	98.5%	Pred. No. 0		
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Gaps 1				
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DB 1245	AGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT	1304
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DEFINITION	Rattus norvegicus neurotrophin mRNA, complete cds.	
ACCESSION	U16845	
VERSION	U16845.1 GI:755184	
KEYWORDS		
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
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	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
REFERENCE	1 (bases 1 to 2040)	
AUTHORS	Struyk, A.F., Canoll, P., Wotfang, J., Rosen, C.L., D'Eustachio, P.	
TITLE	Cloning of neurotrophin defines a new subfamily of differentially	
JOURNAL	expressed neural cell adhesion molecules	
MEDLINE	J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)	
PMID	7831157	
REFERENCE	2 (bases 1 to 2040)	
AUTHORS	Salzer, J.L.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical	
FEATURES	Center, 550 First Avenue, New York, NY 10016, USA	
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RESULT 11

AF282980 1410 bp mRNA linear ROD 01-FEB-2001
LOCUS Mus musculus neurotrimin mRNA, complete cds.
DEFINITION AF282980
ACCESSION AF282980.1 GI:12642539
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1410)
AUTHORS Kim,T.H., Choi,S.C., Kim,J., Jeon,J.W., Kim,K.D. and Lee,S.H.
TITLE Cloning and expression of mouse neurotrimin gene in the developing nervous system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1410)
AUTHORS Kim,T.H., Choi,S.C., Kim,J., Jeon,J.W., Kim,K.D. and Lee,S.H.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea University, 1-5-ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea
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BASE COUNT 369 a 365 c 368 g 308 t
ORIGIN

Query Match 54.2a; Score 910.6; DB 10; Length 1410;
Best Local Similarity 84.6a; Pred. No. 9.2e-231;
Matches 1134; Conservative 0; Mismatches 184; Indels 23; Gaps 9;
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QY 274 CCGCAGGCGGAGAGGCGCCACCTCAGTGTGACACTATTGACAAACCGGGTCACCCGGGTGGC 333
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QY 394 CGTGTCTCTCTGAGCAACACCCAAACGAGTACAGCATGAGATCCAGAACTGGATGT 453
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LOCUS
DEFINITION Sequence 102 from Patent WO03002765.
ACCESSION AX665344
VERSION AX665344.1 GI:29290465
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
REFERENCE
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Patent: WO 03002765-A 102 09-JAN-2003;
JOURNAL Cancer Research Technology Limited (GB)
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RESULT 13
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LOCUS
DEFINITION Sequence 104 from Patent WO03002765.
ACCESSION AX665346
VERSION AX665346.1 GI:29290466
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
REFERENCE
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Patent: WO 03002765-A 104 09-JAN-2003;
JOURNAL Cancer Research Technology Limited (GB)
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AX665348 1140 bp DNA linear PAT 26-MAR-2003
LOCUS Sequence 106 from Patent WO03002765
DEFINITION AX665348
ACCESSION AX665348
VERSION AX665348.1 GI:29290467
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 106 09-JAN-2003;
Cancer Research Technology Limited (GB)
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Best Local Similarity 99.8%; Pred. No. 3.8e-215;
Matches 853; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 861 ACATGACTATGGAACTACACTTGGTGGCTCCACACAGCTGGGCCACACCAATGCCAG 920
Qy 1054 CATCATGCTATTGG 1068
Db 921 CATCATGCTATTGG 935

Search completed: September 11, 2003, 01:36:37
Job time : 8040 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 23:11:32 ; Search time 4332 Seconds
(without alignments)
9419,948 Million cell updates/sec

Title: US-10-017-084A-522
Perfect score: 1679
Sequence: 1 gttgtgtcttcagcaaac.....ataaaagagcaaaaaaa 1679

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum-DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

EST.*
1: em_estba:**
2: em_estnum:**
3: em_estin:**
4: em_estnu:**
5: em_estov:**
6: em_estpl:**
7: em_estro:**
8: em_htc:**
9: gb_est1:**
10: gb_est2:**
11: gb_htc:**
12: gb_est3:**
13: gb_est4:**
14: gb_est5:**
15: em_estfun:**
16: em_estom:**
17: em_gss_hum:**
18: em_gss_inv:**
19: em_gss_pin:**
20: em_gss_vrt:**
21: em_gss_fun:**
22: em_gss_ham:**
23: em_gss_mus:**
24: em_gss_pro:**
25: em_gss_rod:**
26: em_gss_phg:**
27: em_gss_vrl:**
28: gb_gss1:**
29: gb_gss2:**

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1119.4	66.7	1808	11 AK045973	AK045973 Mus muscu
2	1119.4	66.7	1808	11 AK046377	AK046377 Mus muscu
3	733.4	43.7	1033	12 BM807426	BM807426 AGENCOURT
4	720.2	42.9	1083	12 BM809227	BM809227 AGENCOURT

5	674	40.1	865	12	BI666583	BI666583 603291469
6	664.8	39.6	856	13	BU155617	BU155617 AGENCOURT
7	645	38.4	1085	9	AL533026	AL533026 AL533026
8	643	38.3	732	12	BI551784	BI551784 603197479
9	635.2	37.8	1039	10	BE798585	BE798585 601581610
10	628.4	37.4	784	12	BI549918	BI549918 603194765
11	621.2	37.0	870	12	BI913885	BI913885 603182295
12	619.6	36.9	765	14	CD354474	CD354474 UI-M-GMO-
13	611	36.4	737	12	BM797977	BM797977 UI-M-GMO-
14	602.4	35.9	604	9	AW025115	AW025115 WU71H04.X
15	598.8	35.7	602	13	BU741589	BU741589 UI-E-E01-
16	594.8	35.4	770	9	AW117456	AW117456 Xd9a06.X
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18	549	32.7	561	12	BM009450	BM009450 603629962
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25	488	29.1	660	14	BY723873	BY723873 BY723873
26	488	29.1	488	2	HS067401	HS067401 Homo sapi
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31	475.4	28.3	486	9	AI753140	AI753140 cr05g10.X
32	469	27.9	522	12	BI553032	BI553032 603193672
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34	457.4	27.2	524	10	BE014142	BE014142 125737 MA
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43	444.4	26.5	548	10	BE015245	BE015245 127482 MA
44	443.8	26.4	555	12	BI548049	BI548049 603196558
45	439	26.1	440	9	AI318423	AI318423 q059g09.X

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED
AK045973	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230328N06 product:NEUR0TRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.	1808 bp mRNA linear	AK045973	1	GI:26337738	HTC; CAP trapper.	Mus musculus (house mouse)	1	Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	11042159
AK045973	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230328N06 product:NEUR0TRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.	1808 bp mRNA linear	AK045973	1	GI:26337738	HTC; CAP trapper.	Mus musculus (house mouse)	2	Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	11042159

REFERENCE
AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nageoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

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source

1. 1808
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/codon_start=1
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/db_xref="GI:26337739"
/translation="MTIDAKHNSISWAIETGLAALCLFQGVBSGDATPEKAMON VYRGESATYRCTIDNRYVAVHNSITLYAGNKKKCLDPRVLLSNTOFYSIEI ONVDYDSCPTSCVQDNIHPTKTSVHLIVQVSKLVEISSDISINEGNSLISLTIAT GRPEYIVRHISKAVGFVSEDEYLEICGTRGDSGEISCSASNDYAPVRRVKYI VNPPIISEARGTGPVQNGTGLQCEASAVSFQFMDKRLVKGKGVAVENRPF LSKLTFNVSHEIDYGNVTCVASNKLGHNASIMLFGPGVSEVNNCTSRAGCWLPLP LVLHLLHLK"

CDS

BASE COUNT 550 a 431 c 462 g 365 t
ORIGIN
Query Match 66.7%; Score 1119.4; DB 11; Length 1808;
Best Local Similarity 83.1%; Pred. No. 2.9e-146;
Matches 1417; Conservative 0; Mismatches 251; Indels 37; Gaps 11;

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59 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTTCAGAGCAACAC 118
61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGCACAAAAA-----G 108
119 AATCTATCAGGAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 178
109 AAGAAAG 168
179 AAG 238
169 CTCTTGGGCAATCTTCAGGGGCTGGCTGCTGTGTCTCTTCTTCAAGAGAGTGCCTGGG 228
239 CTCTTGGGCAATCTTCAGGGGCTGGGCTGTGTGTCTTCTTCAAGAGAGTGCCTGGG 298
229 CAGGGAGAGTGCCTTCCCAAGAGATGTGACACACGTCGCTCCGCGAGGGGAGAG 288
299 TAGCGGAGATGCCACCTTTCCCAAGAGATGTGACACACGTCGCTCCGCGAGGGGAGAG 358
289 CGGCACCTCAGTGCACATTTAGCAACACCGGGTACCGGGTGGCTGGCTTAAACCGCAG 348
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529 GCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAGAACAA 588
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11076861

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kuchiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Tomita, M., Quackenbush, J., Schriml, L.M., Staehli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Buit, C., Cline, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J.H., Kohtsuki, S., and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

21085660

11217851

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1808)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan. (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-3216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

Location/Qualifiers

FEATURES

Oy	589	TATTAGCCTCACCTGATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACAT	648
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Db	1728	GTGAATCTGGAGAGAAAAA	1752
Db	AK046377	Mus musculus adult male corpora quadrigenina cDNA, RIKEN full-length enriched library, Clone:B30377K17, product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.	
Oy	AK046377	1808 bp mRNA linear HTC 05-DEC-2002	
Db	AK046377	HTC; CAP trapper.	
Oy	AK046377	Mus musculus (house mouse)	
Db	AK046377	Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sclurognathi; Muridae; Murinae; Mus.	
Oy	AK046377	Carninci, P. and Hayashizaki, Y.	
Db	AK046377	High-efficiency full-length cDNA cloning	
Oy	AK046377	Meth. Enzymol. 303, 19-44 (1999)	
Db	AK046377	99279253	
Oy	AK046377	10349636	
Db	AK046377	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
Oy	AK046377	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
Db	AK046377	Genome Res. 10 (10), 1617-1630 (2000)	
Oy	AK046377	20499374	
Db	AK046377	11042159	
Oy	AK046377	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, I., Hatada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, F., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, M., Ohara, F., Kasukawa, T., Saito, R., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
Db	AK046377	RIKEN integrated sequence analysis (RISA) system: 384-format sequencing pipeline with 384 multicapillary sequencer	
Oy	AK046377	Genome Res. 10 (11), 1757-1771 (2000)	
Db	AK046377	20530913	
Oy	AK046377	11076861	
Db	AK046377	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischnann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staab, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bernaldo, M. F., Brownstein, M. J., Bult, C. N., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, J. P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyohara, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y.	
Oy	AK046377	Functional annotation of a full-length mouse cDNA collection	
Db	AK046377	Nature 409 (6821), 685-690 (2001)	
Oy	AK046377	21085660	
Db	AK046377	11217851	
Oy	AK046377	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
Db	AK046377	Analysis of the mouse transcriptome based on functional annotation	
Oy	AK046377	of 60,770 full-length cDNAs	


```

source
1. 865
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:5310833"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
size-selected for average insert size 2.3 kb and
normalized to 500 ng. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). -Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 250 a 230 c 209 g 176 t
ORIGIN

Query Match 40.1%; Score 674; DB 12; Length 865;
Best Local Similarity 99.9%; Pred. No. 1.5e-85;
Matches 685; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GTTGTGCTTTCAGCAAAACAGTGATTTAAATCTCTTTCACAAAGCTTGAGAGCAACAC 60
DB 50 GTTGTGCTTTCAGCAAAACAGTGATTTAAATCTCTTTCACAAAGCTTGAGAGCAACAC 109
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 110 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 169
QY 121 AAGAAAAAAATCATGAAACCATCCAGCAAAATGCAATTTCTCTTGGCAAT 180
DB 170 AAGAAAAAAATCATGAAACCATCCAGCAAAATGCAATTTCTCTTGGCAAT 229
QY 181 CTTACGGGGCTGGCTGCTCTGCTCTTCCAGAGAGTGCCCGGAGGGGAGAGCCACCTCAG 240
DB 230 CTTACGGGGCTGGCTGCTCTGCTCTTCCAGAGAGTGCCCGGAGGGGAGAGCCACCTCAG 289
QY 241 CACCTTCCCAAGCTATGACACAGCTGAGGTCGCGGAGGGGAGAGCCACCTCAG 300
DB 290 CACCTTCCCAAGCTATGACACAGCTGAGGTCGCGGAGGGGAGAGCCACCTCAG 349
QY 301 GTGCACATTTGACACCGGGTACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTA 360
DB 350 GTGCACATTTGACACCGGGTACCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTA 409
QY 361 TGCTGGGAATGACAAGTGGCTGGATCTCGCTGGTCTTCTGTGACACACCCCAAC 420
DB 410 TGCTGGGAATGACAAGTGGCTGGATCTCGCTGGTCTTCTGTGACACACCCCAAC 469
QY 421 GCAGTACAGCATCGAGATCCAGACGCTGGATGTGTATGAGAGGGCCCTTACACCTGCTC 480
DB 470 GCAGTACAGCATCGAGATCCAGACGCTGGATGTGTATGAGAGGGCCCTTACACCTGCTC 529
QY 481 GTGCACAGACACACCCCAAGAGCTCTAGGTCACCTCATTTGTGCAATCTCTCC 540
DB 530 GTGCACAGACACACCCCAAGAGCTCTAGGTCACCTCATTTGTGCAATCTCTCC 589
QY 541 CAATATTTGACATTTCTTCAATATCTCANTATAGAGGAAC-AATATAGGCTCA 599
DB 590 CAATATTTGACATTTCTTCAATATCTCANTATAGAGGAACAAATATAGGCTCA 649
QY 600 CTTGATAGCACTGTGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAG 659
DB 650 CTTGATAGCACTGTGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAG 709
QY 660 CGGTGGCTTTGTGAGTGAAGACGAA 685
DB 710 CGGTGGCTTTGTGAGTGAAGACGAA 735

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RESULT 6
BUI55617
LOCUS
DEFINITION AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
5', mRNA sequence.
ACCESSION BUI55617
VERSION BUI55617.1
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases from 856)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cyapbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM13527 row: m column: 16
High quality sequence stop: 593.
FEATURES
Location/Qualifiers
1. 856
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:6166839"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 217 a 228 c 239 g 172 t
ORIGIN

Query Match 39.6%; Score 664.8; DB 13; Length 856;
Best Local Similarity 97.6%; Pred. No. 2.9e-84;
Matches 728; Conservative 0; Mismatches 12; Indels 6; Gaps 5;

QY 214 AGAGTGCCCGTGGCGAGCGAGATGCCACCTTCCCAAGCTATGACAAAGCTGACGCT 273
DB 94 AGAGTGCCCGTGGCGAGCGAGATGCCACCTTCCCAAGCTATGACAAAGCTGACGCT 153
QY 274 CCGCAGGGGAGAGCGCCACCTTCAGGTGCTACTTTCACAAACCGGTACCCGGGTGCG 333
DB 154 CCGCAGGGGAGAGCGCCACCTTCAGGTGCTACTTTCACAAACCGGTACCCGGGTGCG 213
QY 334 CTGGCTTAACCGCAGCACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 393
DB 214 CTGGCTTAACCGCAGCACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 273
QY 394 CTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 453
DB 274 CTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 333
QY 454 GTATGACAGAGGCGCTTACACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 513
DB 334 GTATGACAGAGGCGCTTACACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 393
QY 514 GTTCCACCTCATTTGTGCAAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 573
DB 394 GTTCCACCTCATTTGTGCAAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 453
QY 574 TAATGAAGGGAACATATTTAGCTCTACCTTCCATAGCACTGCTAGACAGAGCTACGCT 633

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DB 454 TAATGAAGGAGAACAAATATAGCCTCACCTGATAGCACTGGTAGACAGAGCCTACGGT 513
QY 634 TACTTGGAGACATCTCTCCCAAGCGGTTGGCTTGTGAGTGAAGAGCAATATCTTGA 693
DB 514 TACTTGGAGACATCTCTCCCAAGCGGTTGGCTTGTGAGTGAAGAGCAATATCTTGA 573
QY 694 AATTGAGGATCACCCGGGAGCAGTCAGGGGAGTCAAGAGTCAAGTGGCTCCATGACGT 753
DB 574 AATTGAGGATCACCCGGGAGCAGTCAGGGGAGTCAAGAGTCAAGTGGCTCCATGACGT 633
QY 754 GGCSCGCCGCTGGTACGGAGAGTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 813
DB 634 GGCSCGCCGCTGGTACGGAGAGTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 693
QY 814 AGCCAAAGGATACAGGTGT-CCCGTGGGACAAAGGGGACACTGCAG-TGTGAGGCTCA 871
DB 694 AGCCAAAGGATACAGGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAACCTCA 753
QY 872 GCAGTCCCTCAGCAG-AATTCAGTGTGACAGGATG-ACAAAGACTGATT--GAGG 927
DB 754 GCAGTCCCTCAGCAGAAATTCAGTGTGACAGGATGACCAAGACTGATTGGAAGG 813
QY 928 AAGAAGAGGAGTGAAGTGAAGAAACA 953
DB 814 AAAAAAGGGGTGAAGAGGGGAAAA 839

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RESULT 7

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AL533026 1085 bp mRNA linear EST 23-MAY-2003
LOCUS AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN005YD20 5-PRIME, mRNA sequence.
ACCESSION AL533026
VERSION AL533026.2 GI:31070858
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE

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1. (bases 1 to 1085)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12796519.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 Evry cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6387.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DN005DB10QPL&cluster=6387.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DN005DB10QPL.
Location/Qualifiers
1. 1085
/organism="Homo sapiens"
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/clone="CS0DN005YD20"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/notes="Organ: Brain; Vector: pcMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pcMVSPORT 6
vector. Library was not normalized."

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FEATURES

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BASE COUNT 318 a 261 c 263 g 234 t
ORIGIN
DEFINITION 60319749F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:527115 5',
LOCUS BI551784 732 bp mRNA linear EST 05-SEP-2001
DEFINITION 60319749F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:527115 5',

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Query Match 38.4%; Score 645; DB 9; Length 1085;
Best Local Similarity 86.8%; Pred. No. 1.6e-81;
Matches 806; Conservative 1; Mismatches 1; Indels 121; Gaps 4;
QY 531 AAGTATCTCCCAAAATCTAGAGATTCTTCAGATATCTCCATTAATGAAGGGAACAATA 590
DB 160 AAGTATCTCCCAAAATCTAGAGATTCTTCAGATATCTCCATTAATGAAGGGAACAATA 219
QY 591 TTAGCTTCACTGCATAGTACTGCTAGCAGAGAGCCCTACGTTTACTTTGAGACATCT 650
DB 220 TTAGCTTCACTGCATAGTACTGCTAGCAGAGAGCCCTACGTTTACTTTGAGACATCT 279
QY 651 CTCCCAAGCGGTTGGCTTTGTGAGTGAAGAGCAATCTTGGAAATTCAGGCATCACCC 710
DB 280 CTCCCAAGCGGTTGGCTTTGTGAGTGAAGAGCAATCTTGGAAATTCAGGCATCACCC 339
QY 711 GGGAGCAGTCAGGGGACTGAGAGTGCAGTGCCTCCAAATGAGTGGCGCGCGCTGGTAC 770
DB 340 GGGAGCAGTCAGGGGACTGAGAGTGCAGTGCCTCCAAATGAGTGGCGCGCGCTGGTAC 399
QY 771 GGGAGTAAAGTCAAGTCAAGTATCCACCATATCTTTAGAGAGCCAGGGTACAGGTG 830
DB 400 GGGAGTAAAGTCAAGTCAAGTATCCACCATATCTTTAGAGAGCCAGGGTACAGGTG 459
QY 831 TCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAAT 890
DB 460 TCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAAT 519
QY 891 TCCAGTGGTACAAAGGATGACAAAA 914
DB 520 TCCAGTGGTACAAAGGATGACAAAAAGAGCTGAAATCTCATTACAGTTTGGTATGATGGG 579
QY 915 914
DB 580 AAAGCTTCTCCCTCCCATGGTGGAGCAATGTGTCAAAAGCGGACAGTCAATCAGCCT 639
QY 915 914
DB 640 GACTTGTCTCGAGAAATCTCCCGACTGATTGAGGAGAAAGGGGTGAAGTGAAGAAC 699
QY 953 AGACCTTCTCTCAAAACATCTTCTCAATCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1012
DB 700 AGACCTTCTCTCAAAACATCTTCTCAATCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 759
QY 1013 ACTTGTGCTCTCCCAAGCAGTGGGCGCACCAATGTCAGCATCATCTATTGTTGCTCA 1072
DB 760 ACTTGTGCTCTCCCAAGCAGTGGGCGCACCAATGTCAGCATCATCTATTGTTGCTCA 819
QY 1073 GGGCGCTCAGGAGGTGAGCAAGCGCAGCTCGAGAGGGGAGGCTCGCTGCTGCTGCTG 1132
DB 820 GGGCGCTCAGGAGGTGAGCAAGCGCAGCTCGAGAGGGGAGGCTCGCTGCTGCTGCTG 879
QY 1133 CTTCTCTCTGCTTCTGCTCTCTCAAAATTTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGG 1192
DB 880 CTTCTCTCTGCTTCTGCTCTCTCAAAATTTTGTGAGTGGTGGTGGTGGTGGTGGTGG 938
QY 1193 GAAAGCTGCTCCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1252
DB 939 GAAAGCTGCTCCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 997
QY 1253 ATCAGATATATCAAAATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1312
DB 998 ATCAGATATATCAAAATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1057
QY 1313 AGGGGAACAAAGATACTTTGGGGGGA 1341
DB 1058 AGGGG-ACAAAGAAATACTTTGGGGGGA 1085

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RESULT 8

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BI551784 732 bp mRNA linear EST 05-SEP-2001
LOCUS BI551784
DEFINITION 60319749F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:527115 5',

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mRNA sequence.
BI551784.1 GI:15439096
VERSION BI551784.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL 1 (bases 1 to 732)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Cloned distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11699 row: m column: 20
High quality sequence stop: 732.
Location/Qualifiers
1. 732
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5277115"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH-MGC_95"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
size-selected for average insert size 2.5 kb and
normalized to 10^5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health) Note: this is a NIH-MGC Library."
BASE COUNT 218 a 191 c 172 g 150 t
ORIGIN
Query Match 38.3%; Score 643; DB 12; Length 732;
Best Local Similarity 99.4%; Pred. No. 3.6e-81;
Matches 676; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
Oy 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAGCTTGAGAGCAAC 60
Db 54 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAGCTTGAGAGCAAC 113
Oy 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 119
Db 114 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 173
Oy 120 GAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 179
Db 174 GAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 233
Oy 180 TCTTCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239
Db 234 TCTTCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 293
Oy 240 CCACCTTCCCAAGCTATGGACAACTGACGCTCGCGGAGGGGAGAGCGCCACCTCA 299
Db 294 CCACCTTCCCAAGCTATGGACAACTGACGCTCGCGGAGGGGAGAGCGCCACCTCA 353
Oy 300 GGTGCATATTGACAAAGCGGTGTCACCGGGTGGCTGCTGCTGCTGCTGCTGCTG 359
Db 354 GGTGCATATTGACAAAGCGGTGTCACCGGGTGGCTGCTGCTGCTGCTGCTGCTG 413

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360 ATGCTGGGAATGACAAGTGGTGGCTCGGTGCTTCTTCTAGCAACACCCAAA 419
414 ATGCTGGGAATGACAAGTGGTGGCTCGGTGCTTCTTCTAGCAACACCCAAA 473
420 CGCAGTACAGATCGAGATCCAGACGTGGATGTATGACGAGGGGCTTACACCTGCT 479
474 CGCAGTACAGATCGAGATCCAGACGTGGATGTATGACGAGGGGCTTACACCTGCT 533
480 CGTGTGACAGACAGCAACCCCAAGACCTCTAGGTCCTCCTCATTTGTGCAAGTATCTC 539
534 CGTGTGACAGACAGCAACCCCAAGACCTCTAGGTCCTCCTCATTTGTGCAAGTATCTC 593
540 CGAATATGTAGATATCTTCAGATATCTTCATTAATGAGGAGCAATATAGCCCTCA 599
594 CGAATATGTAGATATCTTCAGATATCTTCATTAATGAGGAGCAATATAGCCCTCA 653
600 CTTGCATAGCACTGGTAGACAGAGCCCTACGTTACTTGG-AGACACATCTCTCCCAA 658
654 CTTGCATAGCACTGGTAGACAGAGCCCTACGTTACTTGGAGAGACACATCTCTCCCAA 713
659 GCGGTGGCTTTGTGAGTGA 678
714 GCGG-TGGCTTTGTGAGTGA 732
RESULT. 9
BE798585 1039 bp mRNA linear EST 20-SEP-2000
LOCUS 601581610F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935955 5'
DEFINITION mRNA sequence.
ACCESSION BE798585
VERSION BE798585
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1039)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLM779 row: d column: 04
High quality sequence stop: 849.
Location/Qualifiers
1. 1039
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="3935955"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="NIH-MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 274 a 271 c 286 g 207 t
ORIGIN
Query Match 37.8%; Score 635.2; DB 10; Length 1039;

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Db 659 CTTGATAGCACTGGTAGCAGAGCTACGGTTACTTGGAGACACCATCTCCCCCAA 718
Qy 657 AAGCGGTGGCTTTGTGA 674
Db 719 AAGCGGTGGCTTCGCGA 736

RESULT 11
B913885 870 bp mRNA linear EST 16-OCT-2001
503183295F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5247550 5'
B913885 mRNA sequence.
DEFINITION B913885
ACCESSION B913885
VERSION B913885
KEYWORDS B913885
SOURCE B913885
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11624 row: m column: 23
High quality sequence stop: 737.
FEATURES
Location/Qualifiers
1..870
/mol_type="mRNA"
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/clone="IMAGE:5247550"
/clone_lib="NIH_MGC_121"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."
BASE COUNT 280 a 200 c 213 g 177 t
ORIGIN
Query Match 37.0%; Score 621.2; DB 12; Length 870;
Best Local Similarity 99.4%; Pred. No. 3.9e-78;
Matches 634; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1042 CACCAATGCCAGCATCATCTATTGGTCCAGGCGCGTCAGGAGTGAGCAACGGCAC 1101
Db 1 CACCAATGCCAGCATCATCTATTGGTCCAGGCGCGTCAGGAGTGAGCAACGGCAC 60
Qy 1102 GTCGAGGAGGCGAGGCTGGCTGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCA 1161
Db 61 GTCGAGGAGGCGAGGCTGGCTGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCA 120
Qy 1162 ATTTGTGTGAGTGCCACTTCCCAACCCCGGGAAGGCTGCCGCCACCAACCAACCAAC 1221
Db 121 A-TTTGTGTGAGTGCCACTTCCCAACCCCGGGAAGGCTGCCGCCACCAACCAACCAAC 179
Qy 1222 ACAACAGCAATGGCAACACCGGACGACCAACCAATCAGATATATACAAATGAATAGAAGA 1281

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Db 180 AACACAGCAATGGCAACACCGGACGAGCAACCAATCAGATATATACAAATGAATAGAAGA 239
Qy 1282 AACACAGCCTCATGGGACAGAAAATTTGAGGAGGGGGAACAAAGAAATACTTTGGGGGAAA 1341
Db 240 AACACAGCCTCATGGGACAGAAAATTTGAGGAGGGGGAACAAAGAAATACTTTGGGGGAAA 299
Qy 1342 AGAGTTTAAAAAAGAAATTTGAAATTTGCTTGCAGATATTTAGGTACAAATGAGTTTTC 1401
Db 300 AAAGTTTAAAAAAGAAATTTGAAATTTGCTTGCAGATATTTAGGTACAAATGAGTTTTC 359
Qy 1402 TTTTCCCAAAAGGGAAGAACACAGACACACCGGCTTGGACCCACTGCAAGCTGCATCGTG 1461
Db 360 TTTTCCCAAAAGGGAAGAACACAGACACACCGGCTTGGACCCACTGCAAGCTGCATCGTG 419
Qy 1462 CAACCTCTTTGTGCTGCTGAGGAGGCTCAGCCTCTCTGCCACAGAGTGCCTCCA 1521
Db 420 CAACCTCTTTGTGCTGAGGAGGCTCAGCCTCTCTGCCACAGAGTGCCTCCA 479
Qy 1522 CFTGGACATCTTGGAGCTGCCATCCCAATTTCAATCAATCAATCAATCAATCAATCAAT 1581
Db 480 CFTGGACATCTTGGAGCTGCCATCCCAATTTCAATCAATCAATCAATCAATCAATCAAT 539
Qy 1582 GAGACCTTCCGCGCCCAAGCGTGGCGCTGGCGGCACTTTGGTAGACTGTGCCACCGGG 1641
Db 540 GAGACCTTCCGCGCCCAAGCGTGGCGCTGGCGGCACTTTGGTAGACTGTGCCACCGGG 599
Qy 1642 TGTGTTGTGAACGCTGAAATAAAAGAGCAAAAAA 1679
Db 600 TGTGTTGTGAACGCTGAAATAAAAGAGCAAAAAA 637

RESULT 12
CD354474 765 bp mRNA linear EST 29-MAY-2003
LOCUS CD354474
DEFINITION UI-M-GMO-cgd-q-16-0-UI-r1 NIH_BMAP_GMO Mus musculus cDNA clone
IMAGE: 30361215 5', mRNA sequence.
ACCESSION CD354474
VERSION CD354474
KEYWORDS EST
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 765)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousef1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pVX-5.
Location/Qualifiers
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/clone_lib="NIH_BMAP_GMO"
/note="Organ: Brain; Vector: pVX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

```

1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fractionation ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-asc vector. The library tag sequence located between the Not I site and the polyA tail is GCAACTCAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., Program coordinator."

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DB	721	TTC 723			

RESULT 13

BM679797/c
LOCUS
DEFINITION
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UI-E-EJ0-ain-k-01-0-UI 3', mRNA sequence.
ACCESSION
BM679797
VERSION
BM679797.1 GI:18989693
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
AUTHORS
TITLE
Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL
MEDLINE
PUBMED
COMMENT
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seq primer: M13 forward
POLYA=yes
Location/Qualifiers
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/clone_lib="UI-E-EJ0"
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TAG_LIB=UI-E-EJ0
TAG_SEQ=AGATCAGA"
BASE COUNT
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ORIGIN
Query Match
Best Local Similarity 94.4%; Pred. No. 1.1e-76;
Matches 690; Conservative 0; Mismatches 5; Indels 36; Gaps 4;
OY 983 AATGCTCTGACATGACTATGGGAACTACACTTGGTGGCTCCCAACAGCTGGGCCAC 1042

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Qy	1190	CGGGAAGGCTCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	1249
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Qy	1250	CCAACTAGATATATACAAATGAAATTAGAGAAACACACAGCTCATGGGACAGAAATTTGA	1309
Db	439	CCAACTAGATATATACAAATGAAATTAGAGAAACACACAGCTCATGGGACAGAAATTTGA	380
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Qy	1430	CCGGCTTGGACCACTGCAGCTGCATGCTGCACCTCTTTGGTGCAGTGTGGGCAG	1489
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Db	79	CGGGCACTTTGTAGACTGTGCCAACCAGCGGCTGTGTGTGAAAGCTGAATTAAGA	20
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Db	19	GCAAAAAATAA 9	

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 22:48:16 ; Search time 570 seconds
(without alignments)
7951.503 Million cell updates/sec

Title: US-10-017-084A-522
Perfect score: 1679
Sequence: 1 gttgttccttcagcaaac.....ataaaagagcaaaaaaa 1679

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs. 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing: first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1679	100.0	1679	22	AAS21431 Human cDNA sequenc
4	1679	100.0	1679	22	AAC67037 Nucleotide sequenc
5	1679	100.0	1679	24	ABL95588 Human angiogenesis
6	1679	100.0	1679	24	ABL88099 Human PRO337 cDNA
7	1679	100.0	1679	24	ABK33598 cDNA encoding huma
8	1679	100.0	1679	25	ACA60326 Novel human secret

9	1679	100.0	1679	25	ACA03790 cDNA encoding huma
10	1679	100.0	1679	25	ACA04211 Human cDNA encodin
11	1679	100.0	1679	25	ACA05116 Novel human secret
12	1679	100.0	1679	25	ACA04996 Novel human secret
13	1679	100.0	1679	25	ABX89328 DNA encoding novel
14	1679	100.0	1679	25	ABX92696 cDNA encoding novel
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18	1509.8	89.9	1873	22	ABK49272 Human Kruppel asso
19	1457	86.8	1678	22	ABX78669 Human polyucleoti
20	1432.8	85.3	1839	22	ABX76448 Lung cancer-associ
21	1315	78.3	1690	22	AAZ59655 Human polyucleoti
22	1032	61.5	1032	21	AAZ47892 Human protein enco
23	939	55.9	939	21	AAZ47894 Human protein enco
24	803.8	47.9	832	21	AAA44536 Human secreted exp
25	540.8	32.2	3069	14	AAO51015 Rat oploid recepto
26	523	31.1	2179	14	AAO51017 Rat oploid recepto
27	523	31.1	12337	14	AAO51016 Human EST DNA2301
28	503	30.0	503	20	AAZ34325 Human PRO337 EST p
29	503	30.0	503	21	ABX92697 Human polyucleoti
30	503	30.0	503	25	ABX92697 Human polyucleoti
31	491.2	29.3	537	22	AAC91321 Spinal cord tissue
32	441.2	26.3	452	22	AAF93346 DNA encoding novel
33	396	23.6	484	23	AAZ78035 Human limbic syste
34	343.8	20.5	1411	24	AAZ50356 Rat LAMP coding se
35	343	20.4	1238	17	AAZ42080 Human cDNA #560 di
36	341.6	20.3	1195	25	ABX63560 Human LAMP residu
37	340.6	20.3	924	17	AAZ42084 Human LAMP residu
38	340.6	20.3	977	17	AAZ42079 Human LAMP coding se
39	340.6	20.3	1014	17	AAZ42086 Human LAMP residu
40	338.6	20.2	861	17	AAZ42082 Human mature LAMP
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ALIGNMENTS

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AC AAZ34324;

XX 07-DEC-1999 (first entry)

XX Human PRO337 nucleotide sequence.

DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;

XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;

XX secreted protein; transmembrane protein; ss.

OS Homo sapiens.

XX MO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1998; 98US-0077450.

XX 11-MAR-1998; 98US-0077632.

XX 11-MAR-1998; 98US-0077641.

XX 12-MAR-1998; 98US-0077791.

XX 13-MAR-1998; 98US-0078004.

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 XX AAC78590;
 AC AAC78590;
 DT 08-FEB-2001 (first entry)
 XX Human PRO337 nucleotide sequence SEQ ID NO:522.
 DE Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KW expressed sequence tag; detection; cancer; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200053756-A2.
 PD 14-SEP-2000.
 XX 18-FEB-2000; 2000WO-US04341.
 XX 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US28565.
 PR 30-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
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 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerfilsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI: 2000-611443/58.
 DR P-PSDB; A3844329.
 XX Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities.
 XX Claim 2, Fig 221; 636pp; English.
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

XX	Sequence	1679 BP	498 A	432 C	419 G	330 T	0 other
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QY	301	GTGCACATATTGACAAACCGGCTCACCCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTTA	360				
DB	301	GTGCACATATTGACAAACCGGCTCACCCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTTA	360				
QY	361	TGCTGGGAATGACAAAGTGGTCCCTGGATCTCGCTGGTCTCTTGAGCAACACCCAAAC	420				
DB	361	TGCTGGGAATGACAAAGTGGTCCCTGGATCTCGCTGGTCTCTTGAGCAACACCCAAAC	420				
QY	421	GCAGTACACATCAGATCCAGAACGTGGATGTGATCAGCAGGGCCCTTACACCTGCTC	480				
DB	421	GCAGTACACATCAGATCCAGAACGTGGATGTGATCAGCAGGGCCCTTACACCTGCTC	480				
QY	481	GGTGCGAGACACACACCAAGACCTTAGGTCCACCTCATCTGCAAGTATCTCC	540				
DB	481	GGTGCGAGACACACACCAAGACCTTAGGTCCACCTCATCTGCAAGTATCTCC	540				
QY	541	CAAAATGTAGAGATTTCTTCAGATATCTCCATTAATAGAGGAAACAAATATTAGCTCTAC	600				
DB	541	CAAAATGTAGAGATTTCTTCAGATATCTCCATTAATAGAGGAAACAAATATTAGCTCTAC	600				
QY	601	CTGCATAGCACTGTGTAGACAGAGCTTACGGTTACTTTGGAGACACATCTCTCCCAAGC	660				
DB	601	CTGCATAGCACTGTGTAGACAGAGCTTACGGTTACTTTGGAGACACATCTCTCCCAAGC	660				
QY	661	GGTTGGCTTTGTGACTGAAGACGAATATCTTGGAAATTTACGGGCATCACCCGGGAGAGTCT	720				
DB	661	GGTTGGCTTTGTGACTGAAGACGAATATCTTGGAAATTTACGGGCATCACCCGGGAGAGTCT	720				
QY	721	AGGGGACTAGAGTGCAGTGCCTCCATGACGTGGCGCGCCGCTGGTACGAGAGATAA	780				
DB	721	AGGGGACTAGAGTGCAGTGCCTCCATGACGTGGCGCGCCGCTGGTACGAGAGATAA	780				
QY	781	GGTCACCGTGAATATCCACCATATCTTCAGAAAGCAAGGAGTACAGTCTCCCGTGGG	840				
DB	781	GGTCACCGTGAATATCCACCATATCTTCAGAAAGCAAGGAGTACAGTCTCCCGTGGG	840				
QY	841	ACAAAGGGGACATGCAAGTGTGAAGCCCTCAGCAGTTCCTCCACAGAAATTCAGTGGTA	900				
DB	841	ACAAAGGGGACATGCAAGTGTGAAGCCCTCAGCAGTTCCTCCACAGAAATTCAGTGGTA	900				
QY	901	CAAGGATGCAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTT	960				
DB	901	CAAGGATGCAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTT	960				
QY	961	CCTCTCAAACACTCATCTCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGGCT	1020				
DB	961	CCTCTCAAACACTCATCTCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGGCT	1020				

961 CCTCTCAAACACTCATCTCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGGCT 1027
 1021 GGCTTCCAAACAGCTGGGCGCACACCAATGCCAGCATCTGCTATTTGGTCCAGGGCGCT 1087
 1021 GGCTTCCAAACAGCTGGGCGCACACCAATGCCAGCATCTGCTATTTGGTCCAGGGCGCT 1087
 1081 CACGAGGTGAGCAACCGGCAAGCTGAGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCT 1140
 1081 CACGAGGTGAGCAACCGGCAAGCTGAGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCT 1140
 1141 GGTCTTGCACCTGCTCTCAAAATTTTGATGTGAGTGCCACTTCCCAACCCGGGAAAGCT 1200
 1141 GGTCTTGCACCTGCTCTCAAAATTTTGATGTGAGTGCCACTTCCCAACCCGGGAAAGCT 1200
 1201 GCGGCGACACACACACCAACACACAGCAATGGCAACACCGAGACAGCAACCAATCAGATA 1266
 1201 GCGGCGACACACACACCAACACAGCAATGGCAACACCGAGACAGCAACCAATCAGATA 1266
 1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
 1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
 1321 AAAGATACTTTGGGGGAAAGAGTGTAAAAAAGAAATTTGAAAAATTTGCCCTTGCAGATA 1380
 1321 AAAGATACTTTGGGGGAAAGAGTGTAAAAAAGAAATTTGAAAAATTTGCCCTTGCAGATA 1380
 1381 TTTAGGTACAATGGAGTTTCTTTTCCAAACCGGAAGAACACAGACACACACCCGGCTTGA 1440
 1381 TTTAGGTACAATGGAGTTTCTTTTCCAAACCGGAAGAACACAGACACACACCCGGCTTGA 1440
 1441 CCACCTGCAAGCTGCATCTGTGCAACCTCTTTTGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
 1441 CCACCTGCAAGCTGCATCTGTGCAACCTCTTTTGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
 1501 TCTGCCACACAGATGCCCCACCTGGAACATTTCTGGAGCTGGCCATCCCAAAATTCAAATCA 1560
 1501 TCTGCCACACAGATGCCCCACCTGGAACATTTCTGGAGCTGGCCATCCCAAAATTCAAATCA 1560
 1561 GTCCATAGAGAGGACACATGAGACCTTCCGCGCCCAAGCTGCGCTGCGGGCACTTTG 1620
 1561 GTCCATAGAGAGGACACATGAGACCTTCCGCGCCCAAGCTGCGCTGCGGGCACTTTG 1620
 1621 GTAGACTGTGCCACACGGGCTGTGTGTGAACCTGTGAACCTGTGAACCTGTGAACCTGTGA 1679
 1621 GTAGACTGTGCCACACGGGCTGTGTGTGAACCTGTGAACCTGTGAACCTGTGAACCTGTGA 1679

RESULT 3
 AAS21431
 ID AAS21431 standard, cDNA, 1679 BP

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PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 20-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04342.
PR 24-FEB-2000; 2000WO-US04514.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05061.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX WPI: 2001-408281/43.
XX P-PSDB; AAU12359.
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
XX other PRO polypeptides, link bioactive molecules to cells expressing,
XX PRO polypeptides, and detect the presence of mammalian tumours e.g.
XX lung, breast, prostate, cervical
XX Claim 3; Fig 375; 813pp; English.
XX AAS21244-AAS21518 encode for novel human secretory and transmembrane
XX PRO polypeptides. The PRO polypeptides are useful to detect other
XX PRO polypeptides, to link bioactive molecules to cells expressing
XX PRO polypeptides, to modulate biological activities of cells expressing
XX PRO polypeptides, and to detect the presence of mammalian lung, colon,
XX breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX polypeptide expression in a cell sample to that in a control sample.
XX Some of the 275 sequences are also useful to stimulate the release of
XX tumour necrosis factor-alpha (TNF-alpha) from human blood, the
XX proliferation or differentiation of chondrocytes, the proliferation or
XX gene expression in pericyte cells, the release of proteoglycans from
XX cartilage, the proliferation of inner ear utricular supporting cells or
XX of T-lymphocytes, the release of a cytokine from peripheral blood
XX monocytes (PMNCs), or the proliferation of endothelial cells. Some of
XX the PRO polypeptides may modulate glucose or free fatty acid uptake by
XX skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
XX to factor VIIA. The PRO polypeptides can be used in assays to identify
XX molecules involved in binding interactions. The polynucleotides encoding
XX PRO polypeptides can be used to generate probes, antisense RNA/DNA,
XX transgenic or knock out animals and can be used in gene therapy.
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
XX Query Match 100.0%; Score 1679; DB 22; Length 1679;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTGAGAGCAACAC 60
DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTGAGAGCAACAC 60
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

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OY	241	CACCTTCCCAAGCTATGACACAGCTGAGCGTCCGCGAGGGGAGAGCGCCACCCCTCAG	300
Db	241		
OY	301	GTGCACTATTGACAAACCGGTCACCGGTCGCGCTGGCTTAAACCGCAGCACCATCTCTTA	360
Db	301		
OY	361	TGCTGGGAATGACAAAGTGGTCCCTGGATCCTCGCGTGTCTCTTGAGCAACACCCAAAC	420
Db	361		
OY	421	GCAGTACAGCATCGAGATCCAGAACGCTGGATGTATGACGAGGGCCCTTACACCTGGTC	480
Db	421		
OY	481	GGTCAGACAGAACACCAACCAAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCC	540
Db	481		
OY	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600
Db	541		
OY	601	CTCATAGCAACTGGTAGACACAGAGCTACGGTTACTTTGGAGACATCTCTCCCAAGC	660
Db	601		
OY	661	GTTGGCTTTGTGAGTGAAGACCAATACCTTGAATTCAGGGCATCACCGGAGCAGTC	720
Db	661		
OY	721	AGGGACTAGAGTGCAGTGCCTCCAAATACCTGCGCGCCCGCTGGTACGGAGATGAA	780
Db	721		
OY	781	GTCACCGTGAACACTACCACTACATTTTCAGAGCCAAAGGTACAGGTGTCCTCCGCGG	840
Db	781		
OY	841	ACAAAAGGGACACTGTCAGTGTGAAGCCTCAGCAGTCCCTTCAGCAGAAATTCAGTGGTA	900
Db	841		
OY	901	CAAGGATGACAAAAGACTGATTGAAGGAAGAAAGGGGTGAAAGTGAAGTGAAGACACCTTT	960
Db	901		
OY	961	CTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTGGT	1020
Db	961		
OY	1021	GGCTTCAACAGCTGGGCCACACCAATGCCAGCATCATCTATTTGGTCCAGGCGCGT	1080
Db	1021		
OY	1081	CAGCAGGTGACCAACCGCAGCTCGAGGAGCGAGCTGTCTGTGCTGCTCTCTCTTCT	1140
Db	1081		
OY	1141	GGTCTGACCTGCTCTCAAAATTTTGTATGTAGTGGCACTTCCCAACCCGGGAAGGCT	1200
Db	1141		
OY	1201	GCGCCACACCAACCAACAGCAATGGCAACACCGCAGCAACCAATCAGATA	1260
Db	1201		
OY	1261	TATACAAATGAAATAGAGAAACACAGCTCTATGGAGACAGAAATTTGAGGAGGGGAC	1320
Db	1261		
OY	1321	AAAGTACTTTGGGGGAAAAGAGTTTAAAGAGAAATTTGAAATTCCTTCAGATA	1380
Db	1321		

Db	1321	AAAGAAATCTTTGGGGGAAAAGAGTTTAAAGAGAAATTTGAAATTCCTTCAGATA	1380
OY	1381	TTTAGGTACAATGAGGTTTCTTTTCCCAACGGGAAGAACACAGACACACCGGCTTGGGA	1440
Db	1381		
OY	1441	CCCACTGCAAGCTGCATCTGCAACCTCTTTTGTGCGCAGTGTGGGCAAGGGCTCAGCCTC	1500
Db	1441		
OY	1501	TCGTGCCACAGAGTGGCCCCAGCTGTGAACATTTCTGGAGCTGGCCATCCCAATTCATCA	1560
Db	1501		
OY	1561	GTCCATAGACAGCAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGCACCTTG	1620
Db	1561		
OY	1621	GTAGACTGTGCTCCACCGCGCTGTCTGTGAACCTGAAATTAAGAGAGCAAAAAA	1679
Db	1621		

RESULT 5
ABL95588 standard; cDNA; 1679 BP.
XX ABL95588;
XX
DT 19-JUL-2002 (first entry)
XX
Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
cardiant; cytosolic; antiangiogenic; hypotensive; vulnerary;
antiarteriosclerotic; gene; ss.
XX Homo sapiens.
XX
FN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 28-JUL-2000; 2000US-220664P.
PR 02-AUG-2000; 2000WO-US20710.
PR 17-AUG-2000; 2000US-222605P.
PR 23-AUG-2000; 2000WO-US23322.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-070923P.
PR 10-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 22-JAN-2001; 2000WO-US34956.
PR 28-FEB-2001; 2001US-0796498.
PR 01-MAR-2001; 2001WO-US06520.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806589.
PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866026.
 PR 25-MAY-2001; 2001US-0866034.
 PR 30-MAY-2001; 2001MO-US17092.
 PR 30-MAY-2001; 2001MO-US17092.
 PR 30-MAY-2001; 2001MO-US17443.
 PR 01-JUN-2001; 2001MO-US17800.
 PR 20-JUN-2001; 2001MO-US19692.
 PR 28-JUN-2001; 2001MO-US00000.
 XX
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 PI
 XX WPI: 2002-171999/22.
 DR P-PSDB; ABB95450.
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
 PI
 XX Claim 1; Fig 55; 567pp; English.
 PS
 XX The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
 CC
 XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
 SS
 Query Match 100.0%; Score 1679; DB 24; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTCGACAAAGCTTGAGAGCAAC 60
 DB 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTCGACAAAGCTTGAGAGCAAC 60
 QY 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 DB 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 QY 121 AAGAAAAAATCATGAAACCATCCAGCAAGAAATGCAAAATCTATCTCTTGGGCAAT 180
 DB 121 AAGAAAAAATCATGAAACCATCCAGCAAGAAATGCAAAATCTATCTCTTGGGCAAT 180
 QY 181 CTTTCAGGGGCTGGCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 DB 181 CTTTCAGGGGCTGGCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240

QY 241 CACCTTCCCCAAAGCTATGAGCAACGTCGACGGTCCGGCAGGGGAGAGCGCCACCTCAG 300
 DB 241 CACCTTCCCCAAAGCTATGAGCAACGTCGACGGTCCGGCAGGGGAGAGCGCCACCTCAG 300
 QY 301 GTGCACTATTGACAACCGGTGTCACCGGGTGGCTGCTAAACGAGCAGACCATCTCTTA 360
 DB 301 GTGCACTATTGACAACCGGTGTCACCGGGTGGCTGCTAAACGAGCAGACCATCTCTTA 360
 QY 361 TGCTGGGAATGACAAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 TGCTGGGAATGACAAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 GCAGTACAGCATCGAGATCCAGAGCTGATGTGATGAGAGGGCCCTTACACCTGCTC 480
 DB 421 GCAGTACAGCATCGAGATCCAGAGCTGATGTGATGAGAGGGCCCTTACACCTGCTC 480
 QY 481 GGTGAGAGCAGACAACCCCAAGACCTCTAGGCTCCACCTCATTTGTCAAGTATCTCC 540
 DB 481 GGTGAGAGCAGACAACCCCAAGACCTCTAGGCTCCACCTCATTTGTCAAGTATCTCC 540
 QY 541 CAAAATTCGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTAC 600
 DB 541 CAAAATTCGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTAC 600
 QY 601 CTGCATAGCAACTGGTAGAGAGCGCTACGGTTACTTTGAGACACATCTCTCCCAAGC 660
 DB 601 CTGCATAGCAACTGGTAGAGAGCGCTACGGTTACTTTGAGACACATCTCTCCCAAGC 660
 QY 661 GGTGGCTTTGTAGTGAAGAGCATATCTTGAATTTGAGGGCATCCCGGGAGCAGTC 720
 DB 661 GGTGGCTTTGTAGTGAAGAGCATATCTTGAATTTGAGGGCATCCCGGGAGCAGTC 720
 QY 721 AGGGACTACGAGTGCAGTGCCTCCATGACGTGGCGCCGCGCTGGTACGGAGATGAAA 780
 DB 721 AGGGACTACGAGTGCAGTGCCTCCATGACGTGGCGCCGCGCTGGTACGGAGATGAAA 780
 QY 781 GGTACCTGTGAATCTCCACATACATTTTCAAGAACCAAGGGTACAGGTGTCCTCGTGG 840
 DB 781 GGTACCTGTGAATCTCCACATACATTTTCAAGAACCAAGGGTACAGGTGTCCTCGTGG 840
 QY 841 ACAAAGGGGACACTGAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
 DB 841 ACAAAGGGGACACTGAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
 QY 901 CAAGGATGACAAAAGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
 DB 901 CAAGGATGACAAAAGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
 QY 961 CCTCTCAAACTCATCTTCTTCAATGCTCTCTGAACATGACTATGGGAACCTACACTTGG 1020
 DB 961 CCTCTCAAACTCATCTTCTTCAATGCTCTCTGAACATGACTATGGGAACCTACACTTGG 1020
 QY 1021 GGCCTCCAGCAAGCTGGCCACACCAATGCCAGCATCTGCTATTTGGTCCAGGGCGCT 1080
 DB 1021 GGCCTCCAGCAAGCTGGCCACACCAATGCCAGCATCTGCTATTTGGTCCAGGGCGCT 1080
 QY 1081 CAGCAGGTGAGCAACGGCAGCTGCGAGAGGGCAGGTGCTGCTGCTGCTGCTCTTCT 1140
 DB 1081 CAGCAGGTGAGCAACGGCAGCTGCGAGAGGGCAGGTGCTGCTGCTGCTGCTCTTCT 1140
 QY 1141 GGTCTTGACCTGCTTCTCAAAATTTTGTGATGTGAGTGGCACTTCCCAACCCGGGAAAG 1200
 DB 1141 GGTCTTGACCTGCTTCTCAAAATTTTGTGATGTGAGTGGCACTTCCCAACCCGGGAAAG 1200
 QY 1201 GCGCCACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1260
 DB 1201 GCGCCACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1260
 QY 1261 TATCAAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGG 1320
 DB 1261 TATCAAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGG 1320
 QY 1321 AAGAATATCTTGGGGGAAAGAGCTTTTAAAGAAATTTGAAATTTGCCTTGCAGATA 1380

DB 1321 AAAGTAATCTTTGGGGGAAAGAGTTTAAAAAAGAAATGAAATTCCTTGCAGATA 1380
QY 1381 TTTAGTACATGAGTTTCTTTTCCCAACGGGAAGACACACAGCACACCGGGCTTGA 1440
DB 1381 TTTAGTACATGAGTTTCTTTTCCCAACGGGAAGACACACAGCACACCGGGCTTGA 1440
QY 1441 CCACCTGCAAGCTGCATCGTGAACCTCTTTGGTCCAGTGTGGCAAGGCTGAGCTC 1500
DB 1441 CCACCTGCAAGCTGCATCGTGAACCTCTTTGGTCCAGTGTGGCAAGGCTGAGCTC 1500
QY 1501 TCTGCCACAGAGTGGCCCGACGTGAACATCTGGAGCTGGCANTCCCAATTCATCA 1560
DB 1501 TCTGCCACAGAGTGGCCCGACGTGAACATCTGGAGCTGGCANTCCCAATTCATCA 1560
QY 1561 GTCCATAGACGACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
DB 1561 GTCCATAGACGACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
QY 1621 GTAGCTGTCACACGCGCTGTGTGTGAAACGTGAATAAATAAAGACCAAAAAA 1679
DB 1621 GTAGCTGTCACACGCGCTGTGTGTGAAACGTGAATAAATAAAGACCAAAAAA 1679

RESULT 6
ID ABL88099 standard; cDNA; 1679 BP.
XX ABL88099;
XX 16-MAY-2002 (first entry)
XX Human PRO337 cDNA sequence SEQ ID NO:55.
XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
XX vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping; gene; ss.
XX Homo sapiens.
XX OS
XX PN
XX WO200200690-A2.
XX 03-JAN-2002.
XX 20-JUN-2001; 2001WO-US19692.
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-249222P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0865028.
PR 25-MAY-2001; 2001US-0865034.
PR 25-MAY-2001; 2001US-0817092.
PR 30-MAY-2001; 2001WO-US17074.
PR 30-MAY-2001; 2001US-0870374.
PR 01-JUN-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX (GETH) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Paoni NF;
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
XX P-PSDB; ABB84844.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal
XX Claim 2; Fig 55; 565pp; English.
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
Query Match 100.0%; Score 1679; DB 24; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTCACAAAGCTTGAGAGCAAC 60
DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTCACAAAGCTTGAGAGCAAC 60
QY 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATTCACATTTCTTCTTGGCAAT 180
DB 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATTCACATTTCTTCTTGGCAAT 180
QY 181 CTTTCACGGGGCTGGCTCTCTGTCTCTTCCAGAGAGTCCCGTCCAGCGAGATGC 240
DB 181 CTTTCACGGGGCTGGCTCTCTGTCTCTTCCAGAGAGTCCCGTCCAGCGAGATGC 240
QY 241 CACCTTCCCAAGAGCTATGACACGTGACGCTCCGAGGGGAGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGAGCTATGACACGTGACGCTCCGAGGGGAGAGCGCCACCTCAG 300
QY 301 GTGCACATTTGACAAACGGGTCCACCGGGTGGCTTAACCGACACCAATCTCTA 360
DB 301 GTGCACATTTGACAAACGGGTCCACCGGGTGGCTTAACCGACACCAATCTCTA 360

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361 TGCTGGGAATGACAAGTGGTGCCTGGATCTCGCGTGGTCTCTTCTGAGCAACACCCAAAC 420
361 TGCTGGGAATGACAAGTGGTGCCTGGATCTCGCGTGGTCTCTTCTGAGCAACACCCAAAC 420
421 GCAGTCAGCATCGAGATCCAGAACGTGGATGATGATGACGAGGCGCTTACACCTGCTC 480
421 GCAGTCAGCATCGAGATCCAGAACGTGGATGATGATGACGAGGCGCTTACACCTGCTC 480
481 GGTCCAGACAGACACCCCAAGACCTCTAGGTCACCTCATTTGTCGAATATCTCC 540
481 GGTCCAGACAGACACCCCAAGACCTCTAGGTCACCTCATTTGTCGAATATCTCC 540
541 CAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAGGGAACATATATAGCTCAC 600
541 CAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAGGGAACATATATAGCTCAC 600
601 CTGCATAGCACTGGTAGCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
601 CTGCATAGCACTGGTAGCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
661 GGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
661 GGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
721 AGGGACTACGAGTGCAGTGCCTCCTCAATGACGTGGCGCGCGCGTGTACGGAGAGTAA 780
721 AGGGACTACGAGTGCAGTGCCTCCTCAATGACGTGGCGCGCGCGTGTACGGAGAGTAA 780
781 GGTCAACCGTGAATCTCCACCATATCTTTCAGAGGCAAGGTACAGGTGTCCCGTGG 840
781 GGTCAACCGTGAATCTCCACCATATCTTTCAGAGGCAAGGTACAGGTGTCCCGTGG 840
841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTTCCAGTGTGA 900
841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTTCCAGTGTGA 900
901 CAAGGATGACAAAGACTGATTTGAAGAAAGAGGAGGAGTGAAGTGAAGAAAGAGACTTT 960
901 CAAGGATGACAAAGACTGATTTGAAGAAAGAGGAGGAGTGAAGTGAAGAAAGAGACTTT 960
961 CCTCTCAAACTCATCTCTTCAATGTCTGAAATGACTATGGAACATGGAACATCTTGGT 1020
961 CCTCTCAAACTCATCTCTTCAATGTCTGAAATGACTATGGAACATGGAACATCTTGGT 1020
1021 GGCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGCT 1080
1021 GGCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGCT 1080
1081 CAGCGAGTGCAGCAACGGCAGCTCGAGGAGGCGAGCTGCGTCTGCTGCTGCTCTTCT 1140
1081 CAGCGAGTGCAGCAACGGCAGCTCGAGGAGGCGAGCTGCGTCTGCTGCTGCTCTTCT 1140
1141 GGTCTTGACCTGCTCTTCAATTTGATGTGAGTGGCAGCTTCCACCCGGGAAGGCT 1200
1141 GGTCTTGACCTGCTCTTCAATTTGATGTGAGTGGCAGCTTCCACCCGGGAAGGCT 1200
1201 GCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
1201 GCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
1261 TATCAAAATGAATTTAGAGAAACACAGCTCTATGAGCAAGAAATTTGAGGAGGGAAC 1320
1261 TATCAAAATGAATTTAGAGAAACACAGCTCTATGAGCAAGAAATTTGAGGAGGGAAC 1320
1321 AAGAATACCTTTGGGGGAAAAGAGTTTAAAGAAATTTGAAATTTGCTTGCAGATA 1380
1321 AAGAATACCTTTGGGGGAAAAGAGTTTAAAGAAATTTGAAATTTGCTTGCAGATA 1380
1381 TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGCACACCCGGCTTGA 1440
1381 TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGCACACCCGGCTTGA 1440

OY 1441 CCACCTGCAAGCTGCATCTGCAACCTCTTTTGTGTCAGTGTGGCAAGGCTCAGCCTC 1500
DB 1441 CCACCTGCAAGCTGCATCTGCAACCTCTTTTGTGTCAGTGTGGCAAGGCTCAGCCTC 1500
OY 1501 TCTGCCCCACAGAGTGGCCCCACCTGGAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
DB 1501 TCTGCCCCACAGAGTGGCCCCACCTGGAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
OY 1561 GTCCATAGAGACGACAGCAATGACACTTCCGGGCCACAGCTGGCGCTGGGGCACTTTG 1620
DB 1561 GTCCATAGAGACGACAGCAATGACACTTCCGGGCCACAGCTGGCGCTGGGGCACTTTG 1620
OY 1621 GTAGACTGTGCCACACCGGCTGTGTGTGAAAGCTGAATATAAAGACGCAAAAAAAA 1679
DB 1621 GTAGACTGTGCCACACCGGCTGTGTGTGAAAGCTGAATATAAAGACGCAAAAAAAA 1679

RESULT 7
ABK33598
ID ABK33598 standard; cDNA; 1679 BP.
XX
AC ABK33598;
XX
DT 08-MAY-2002 (first entry)
XX
XX cDNA encoding human PRO protein, Seq ID No 125.
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha; gene; ss.
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220605P.
XX 25-JUL-2000; 2000US-220607P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220638P.
XX 25-JUL-2000; 2000US-220664P.
XX 25-JUL-2000; 2000US-220666P.
XX 26-JUL-2000; 2000US-220893P.
XX 28-JUL-2000; 2000WO-US20710.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 15-SEP-2000; 2000US-000000P.
XX 10-NOV-2000; 2000WO-US30873.
XX 28-NOV-2000; 2000US-253646P.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 28-FEB-2001; 2001WO-US06520.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001WO-US17092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX WPI; 2002-172001/22.
XX P-PSDB; AAU83654.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours.
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX
```

PT tumour or liver tumour -
 XX Claim 2; Figure 125; 359pp; English.
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human
 CC PRO protein coding sequences of the invention.
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0%; Score 1679; DB 24; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGTTGAGAGCAAC 60
 DB 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGTTGAGAGCAAC 60
 QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 QY 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAAAATCTATCTCTTGGCAAT 180
 DB 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAAAATCTATCTCTTGGCAAT 180
 QY 181 CTTTCAGGGGCTGGCTGCTGTCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGC 240
 DB 181 CTTTCAGGGGCTGGCTGCTGTCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGC 240
 QY 241 CACCTTCCCAAGCTATGGACACGTGACGGTGCAGGGGAGAGCCACCTCAG 300
 DB 241 CACCTTCCCAAGCTATGGACACGTGACGGTGCAGGGGAGAGCCACCTCAG 300
 QY 301 GTGCACTATTGACACCGGTCACCGGGTGGCTTAAACCGCAGCACCCTCTCA 360
 DB 301 GTGCACTATTGACACCGGTCACCGGGTGGCTTAAACCGCAGCACCCTCTCA 360
 QY 361 TGTGGGATGACAGTGGTGGCTTGGATCTCGGTGTCCTTGTAGCAACACCAAC 420
 DB 361 TGTGGGATGACAGTGGTGGCTTGGATCTCGGTGTCCTTGTAGCAACACCAAC 420
 QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTACGAGGGCCCTTACACCTGCTC 480
 DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTACGAGGGCCCTTACACCTGCTC 480
 QY 481 GGTGCAGACAGAACACCAAGACCTCTAGGGTCCACCTATTGTGCAAGTATCTCC 540
 DB 481 GGTGCAGACAGAACACCAAGACCTCTAGGGTCCACCTATTGTGCAAGTATCTCC 540
 QY 541 CAAATTTGAGAGATTCTTCAGATATCTCATTATGAAGGAAACATATTAGCCTAC 600
 DB 541 CAAATTTGAGAGATTCTTCAGATATCTCATTATGAAGGAAACATATTAGCCTAC 600
 QY 601 CTGCAATGACATGTTAGACAGAGCTAGCTTACTTGGAGACATCTCTCCCAAGC 660
 DB 601 CTGCAATGACATGTTAGACAGAGCTAGCTTACTTGGAGACATCTCTCCCAAGC 660
 QY 661 GGTGTGGCTTTGTGAGTGAAGAGCAATATTGGAATTCAGGGCATACCGGGAGCAGTC 720
 DB 661 GGTGTGGCTTTGTGAGTGAAGAGCAATATTGGAATTCAGGGCATACCGGGAGCAGTC 720

DB 661 GGTGTGGCTTTGTGAGTGAAGAGCAATATTGGAATTCAGGGCATACCGGGAGCAGTC 720
 QY 721 AGGGACTACAGTGCAGTGCCTCCCAATGAGTGGCCCGCCCGTGTGAGGAGTAAA 780
 DB 721 AGGGACTACAGTGCAGTGCCTCCCAATGAGTGGCCCGCCCGTGTGAGGAGTAAA 780
 QY 781 GGTACCGGTGAACATATCCACATACATTTTCAAGACCAAGGTTACAGGTGTCCTCGTGG 840
 DB 781 GGTACCGGTGAACATATCCACATACATTTTCAAGACCAAGGTTACAGGTGTCCTCGTGG 840
 QY 841 ACAAAAGGGGACACTGTCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCACGTGTA 900
 DB 841 ACAAAAGGGGACACTGTCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCACGTGTA 900
 QY 901 CAAGGATGACAAAAGACTGATTGAAGAAAGAAAGGGGTGAAAGTGTGAAACAGACCTTT 960
 DB 901 CAAGGATGACAAAAGACTGATTGAAGAAAGAAAGGGGTGAAAGTGTGAAACAGACCTTT 960
 QY 961 CCTCTCAAAAGCTCATCTCTCAATCTCTCTCAATGAGTATGGAACATACACTTGCCT 1020
 DB 961 CCTCTCAAAAGCTCATCTCTCAATCTCTCTCAATGAGTATGGAACATACACTTGCCT 1020
 QY 1021 GGCCTCCAAAGCTGGCCGACACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
 DB 1021 GGCCTCCAAAGCTGGCCGACACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
 QY 1081 CAGCAGGTGAGCAACGGCAGCAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
 DB 1081 CAGCAGGTGAGCAACGGCAGCAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
 QY 1141 GGTCTTGACCTGCTTCTCAATTTTGTAGTGGCAGTCTCCACCCAGCGGAGGAGGAGG 1200
 DB 1141 GGTCTTGACCTGCTTCTCAATTTTGTAGTGGCAGTCTCCACCCAGCGGAGGAGGAGG 1200
 QY 1201 GCGGCACACACACACACACACAGCAATGGCAACACCGCAGCAGCAACCAATCAGATA 1260
 DB 1201 GCGGCACACACACACACACAGCAATGGCAACACCGCAGCAGCAACCAATCAGATA 1260
 QY 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGAGGAG 1320
 DB 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGAGGAG 1320
 QY 1321 AAAGAAATCTTTGGGGGAAAGAGATTTTAAAGAAAGAAATTTGAAATTTGCAAGATA 1380
 DB 1321 AAAGAAATCTTTGGGGGAAAGAGATTTTAAAGAAAGAAATTTGAAATTTGCAAGATA 1380
 QY 1381 TTTAGTACAAATGAGTCTTTTCCCAAGCGGAGAGCAACAGCAGCAGCAGCAGCAGCAG 1440
 DB 1381 TTTAGTACAAATGAGTCTTTTCCCAAGCGGAGAGCAACAGCAGCAGCAGCAGCAGCAG 1440
 QY 1441 CCCACTGCAAGCTGCATGTCGCAACCTCTTTGGTCCAGTGTGGGAGGAGGAGGAGGAGG 1500
 DB 1441 CCCACTGCAAGCTGCATGTCGCAACCTCTTTGGTCCAGTGTGGGAGGAGGAGGAGGAGG 1500
 QY 1501 TCTGCCACAGAGTGCCTCCACAGTGCAGATTTCTGGAGCTGGCCATCCCAATCAATCA 1560
 DB 1501 TCTGCCACAGAGTGCCTCCACAGTGCAGATTTCTGGAGCTGGCCATCCCAATCAATCA 1560
 QY 1561 GTCCATAGAGACGAAACAGATGAGACCTTCCGGCCCAAGGAGGAGGAGGAGGAGGAGG 1620
 DB 1561 GTCCATAGAGACGAAACAGATGAGACCTTCCGGCCCAAGGAGGAGGAGGAGGAGGAGG 1620
 QY 1621 GTAGACTGTGCCACCGGGTGTGTGTGAAAGCTGAAATTAAGAGAGCAAAAAA 1679
 DB 1621 GTAGACTGTGCCACCGGGTGTGTGTGAAAGCTGAAATTAAGAGAGCAAAAAA 1679

RESULT 8:
 ACA60526 standard; CDNA; 1679 BP.
 XX
 AC ACA60526;
 XX

Qy	121	AGAAAAAAATCATGAAAAACCATCCAGCGCAAAAAATGCACAAATTCATCTCTCTGGGCAAT	180
Db	121	AGAAAAAAATCATGAAAAACCATCCAGCGCAAAAAATGCACAAATTCATCTCTCTGGGCAAT	180
Qy	181	CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGAGTGCCTGTGCGCAGCGGAGATGC	240
Db	181	CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCTGTGCGCAGCGGAGATGC	240
Qy	241	CACCTTCCCAAAAGCTATGGACAACTGACAGCTCCGGCAGGGGAGAGCGCCACCTCAG	300
Db	241	CACCTTCCCAAAAGCTATGGACAACTGACAGCTCCGGCAGGGGAGAGCGCCACCTCAG	300
Qy	301	GTGCACCTATTGACAAACCGGGTTCACCCGGGTGGCCCTGGCTAAACCGCAGCAGCACCCTCTA	360
Db	301	GTGCACCTATTGACAAACCGGGTTCACCCGGGTGGCCCTGGCTAAACCGCAGCAGCACCCTCTA	360
Qy	361	TGCTGGGAATGACAAAGTGGTGCCTGGATCCTCGCTGGTGCCTTCAGCAACAACCAACAAC	420
Db	361	TGCTGGGAATGACAAAGTGGTGCCTGGATCCTCGCTGGTGCCTTCAGCAACAACCAACAAC	420
Qy	421	GCAGTACAGCATCGAGATCCAGAAAGCTGGATGTGTATCAGCAGGGGCCCTTACACCTGCTC	480
Db	421	GCAGTACAGCATCGAGATCCAGAAAGCTGGATGTGTATCAGCAGGGGCCCTTACACCTGCTC	480
Qy	481	GGTGACAGACAAACACCCCAAGACCTTAGGTGCCACCTCAATTTGTCGAAGTATCTCC	540
Db	481	GGTGACAGACAAACACCCCAAGACCTTAGGTGCCACCTCAATTTGTCGAAGTATCTCC	540
Qy	541	CANAATGTGTAGAGATTTCTTCAGATATCTCCATTAATGAGAGGAACANATTATGCGCTCAG	600
Db	541	CANAATGTGTAGAGATTTCTTCAGATATCTCCATTAATGAGAGGAACANATTATGCGCTCAG	600
Qy	601	CTGCATAGCAACTGTAGACAGACGCTACGGTTACTTTGGAGACACATCTCTCCCAAGC	660
Db	601	CTGCATAGCAACTGTAGACAGACGCTACGGTTACTTTGGAGACACATCTCTCCCAAGC	660
Qy	661	GTTTGGCTTTGTAGTGAAGACGANATCTTGGAAATTCAGGGCANATCACCCGGGAGCAGTC	720
Db	661	GTTTGGCTTTGTAGTGAAGACGANATCTTGGAAATTCAGGGCANATCACCCGGGAGCAGTC	720
Qy	721	AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCCGTGGTACGGAGAGTAAA	780
Db	721	AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCCGTGGTACGGAGAGTAAA	780
Qy	781	GGTCCACCGTGAACATATCACCATACATTTTCAGAAGCCAAAGGTACAGGTGTCCCCTGGG	840
Db	781	GGTCCACCGTGAACATATCACCATACATTTTCAGAAGCCAAAGGTACAGGTGTCCCCTGGG	840
Qy	841	ACAAAAGGGGACATGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGGTA	900
Db	841	ACAAAAGGGGACATGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGGTA	900
Qy	901	CAAGGATGACAAAACACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT	960
Db	901	CAAGGATGACAAAACACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT	960
Qy	961	CTCTCAAAACTCATCTTCTCAATGCTCTCAACATGACCTATGGGAACCTACACTTGGCT	1020
Db	961	CTCTCAAAACTCATCTTCTCAATGCTCTCAACATGACCTATGGGAACCTACACTTGGCT	1020
Qy	1021	GGCTCCACAGCTGGGCGACACCAATGGCAGCATCATGCTATTGTGCTCAGCGCGGT	1080
Db	1021	GGCTCCACAGCTGGGCGACACCAATGGCAGCATCATGCTATTGTGCTCAGCGCGGT	1080
Qy	1081	CAGCAGGTGACACAGCGCAGTGGAGAGGCGGGCTGGCTGGCTGCTGCTCTCTCT	1140
Db	1081	CAGCAGGTGACACAGCGCAGTGGAGAGGCGGGCTGGCTGGCTGCTGCTCTCTCTCT	1140
Qy	1141	GGTCTTGACACTGCTTCTCAAAATTTTGTAGTGGCAGCTTCCCAACCCGGGAAAGGCT	1200
Db	1141	GGTCTTGACACTGCTTCTCAAAATTTTGTAGTGGCAGCTTCCCAACCCGGGAAAGGCT	1200
Qy	1201	GCCGCCACCAACCAACCAACAGCAGATTTGGCAACACCGACACCAACCAACCAATCAGATA	1260

DECLASSIFIED

RESULT 9
ACR03700

ACA03790
ID ACA03790 standard::cDNA: 1679 BP

XX
AC
ACA03790.AC
XX
ACA03750;

DT 23-MAY-20

XX
XX

DE yy cdna encoding human PRO polypeptide #188.

Human: PRO polypeptide: secreted and transmembrane protein:

KW tumour necrosis factor- α ; TNF- α ; blood; proliferation; human; PKO polypeptide, secreted and transmembrane protein;

KW
differentiation; chondrocyte; tumour; genetic disorder;

KW cytostatic; gene; ss.

XX
XX

OS Homo sapiens.
yyXX
PN
US2003036180-A1[illegible]

PD 20-FEB-2003

[illegible]

PF 09-MAY-2002; 2002US-0143114.

XX
PB 31-MAR-1997. 97WQ-NS05230

PR	31-MAR-1997;	97WO-US05230
PR	12-JUN-1998:	98WO-US12456

PR	12-JUN-1998;	98WO-US12430
PR	14-JUL-1998;	98WO-US14552

PR 28-AUG-1998; 98WO-US17888.

PR 10-SEP-1998; 98WO-US18824.

PR. 14-SEP-1998; 98WO-US19093.
PR. 14-SEP-1998; 98WO-US19094.
PR. 14-SEP-1998; 98WO-US19094.

PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177

PR 14-SEP-1998; 98WO-US19177
PR 16-SEP-1998; 98WO-US19330

PR · 17-SEP-1998;
98WO-US19437.

PR. 07-OCT-1998; 98WO-US21141.

PR 29-OCT-1998; 98WO-US22991.

98WO-US22992.
29-OCT-1998;
98WO-US22992.
20-NOV-1998.
98WO-US24855

PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108

PR	01-DEC-1998;	98WO-US23108.
PR	05-JAN-1999;	99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99WO-US05190.

PR	20-APR-1999	99WO-US08615	14-JUN-2001	2001US-0882636	XX	
PR	14-MAY-1999	99WO-US10735	PR	19-JUN-2001	2001US-0886342	XX
PR	02-JUN-1999	99WO-US12252	PR	21-JUN-2001	2001US-0887879	XX
PR	01-JUL-1999	99WO-US12252	PR	18-JUL-2001	2001US-0908827	XX
PR	08-SEP-1999	99WO-US20594	PR	06-AUG-2001	2001US-0924419	XX
PR	13-SEP-1999	99WO-US20594	PR	09-AUG-2001	2001US-0927796	XX
PR	13-SEP-1999	99WO-US21090	PR	16-AUG-2001	2001US-0931836	XX
PR	13-SEP-1999	99WO-US21547	PR	19-DEC-2001	2001US-0028072	XX
PR	05-OCT-1999	99WO-US23089	XX			
PR	29-NOV-1999	99WO-US28214	PA			
PR	30-NOV-1999	99WO-US28214	XX			
PR	30-NOV-1999	99WO-US28313	XX			
PR	01-DEC-1999	99WO-US28409	PI			
PR	01-DEC-1999	99WO-US28301	PI			
PR	01-DEC-1999	99WO-US28634	PI			
PR	02-DEC-1999	99WO-US28551	XX			
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PR	02-DEC-1999	99WO-US28565	DR			
PR	16-DEC-1999	99WO-US30095	XX			
PR	20-DEC-1999	99WO-US30911	XX			
PR	20-DEC-1999	99WO-US30999	PT			
PR	22-DEC-1999	99WO-US30720	PT			
PR	30-DEC-1999	99WO-US31243	XX			
PR	30-DEC-1999	99WO-US31274	PS			
PR	05-JAN-2000	2000WO-US00219	XX			
PR	06-JAN-2000	2000WO-US00277	XX			
PR	06-JAN-2000	2000WO-US00376	CC			
PR	11-FEB-2000	2000WO-US00365	CC			
PR	18-FEB-2000	2000WO-US04341	CC			
PR	18-FEB-2000	2000WO-US04342	CC			
PR	22-FEB-2000	2000WO-US04414	CC			
PR	24-FEB-2000	2000WO-US04914	CC			
PR	01-MAR-2000	2000WO-US05004	CC			
PR	02-MAR-2000	2000WO-US05601	CC			
PR	02-MAR-2000	2000WO-US05745	CC			
PR	10-MAR-2000	2000WO-US05841	CC			
PR	15-MAR-2000	2000WO-US06319	CC			
PR	20-MAR-2000	2000WO-US07377	CC			
PR	21-MAR-2000	2000WO-US07532	CC			
PR	30-MAR-2000	2000WO-US08439	CC			
PR	17-MAY-2000	2000WO-US13705	CC			
PR	22-MAY-2000	2000WO-US11042	CC			
PR	30-MAY-2000	2000WO-US14941	CC			
PR	02-JUN-2000	2000WO-US15264	CC			
PR	18-JUL-2000	2000WO-US20710	XX			
PR	11-AUG-2000	2000WO-US22031	SQ			
PR	23-AUG-2000	2000WO-US23522				
PR	24-AUG-2000	2000WO-US23328				
PR	08-NOV-2000	2000WO-US30952				
PR	10-NOV-2000	2000WO-US30873				
PR	01-DEC-2000	2000WO-US32678				
PR	28-DEC-2000	2000WO-US34956				
PR	28-FEB-2001	2001WO-US06520				
PR	01-MAR-2001	2001WO-US06666				
PR	25-MAY-2001	2001WO-US17092				
PR	01-JUN-2001	2001WO-US17800				
PR	20-JUN-2001	2001WO-US19692				
PR	22-JUN-2001	2001WO-US20116				
PR	29-JUN-2001	2001WO-US21066				
PR	09-JUL-2001	2001WO-US21735				
PR	20-DEC-2000	2000US-0747259				
PR	28-FEB-2001	2001US-0796498				
PR	09-MAR-2001	2001US-0802706				
PR	14-MAR-2001	2001US-0808699				
PR	22-MAR-2001	2001US-0816744				
PR	05-APR-2001	2001US-0828365				


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Db 301 GTGCACTATTGACACACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGACCAATCTCTA 360
Qy 361 TGTGGGAATGACAAAGTGGTGGCTGGATCTCGCGTGGTCTCTGAGCAACACCAAC 420
Db 361 TGTGGGAATGACAAAGTGGTGGCTGGATCTCGCGTGGTCTCTGAGCAACACCAAC 420
Qy 421 GCATGACAGATCGAGATCCAGAACAGTGGATGTATGACAGAGGCGCTTACACCTGCTC 480
Db 421 GCATGACAGATCGAGATCCAGAACAGTGGATGTATGACAGAGGCGCTTACACCTGCTC 480
Qy 481 GGTGACAGACAGAACACCCCAACAGACCTCTAGGGTCCACCTTATGTGCAAGTATCTCC 540
Db 481 GGTGACAGACAGAACACCCCAACAGACCTCTAGGGTCCACCTTATGTGCAAGTATCTCC 540
Qy 541 CAAATTTGTAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
Db 541 CAAATTTGTAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
Qy 601 CTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
Db 601 CTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
Qy 661 GTTTGGCTTTGTGAGTGAAGAGCAATACTTTGAAATTCAGGGCATCACCGGAGCAGTC 720
Db 661 GTTTGGCTTTGTGAGTGAAGAGCAATACTTTGAAATTCAGGGCATCACCGGAGCAGTC 720
Qy 721 AGGGAGTACGAGTGCAGTGCCTCAATGAGCTGGCGCGCGCGCTGTAGGAGAGTAA 780
Db 721 AGGGAGTACGAGTGCAGTGCCTCAATGAGCTGGCGCGCGCGCTGTAGGAGAGTAA 780
Qy 781 GGTACCGTGAATATCCACATATTCAGAACGAGGATGACAGTGTCCCGCTGG 840
Db 781 GGTACCGTGAATATCCACATATTCAGAACGAGGATGACAGTGTCCCGCTGG 840
Qy 841 ACAAGGGGACACTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAAGTTCAGTGTGA 900
Db 841 ACAAGGGGACACTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAAGTTCAGTGTGA 900
Qy 901 CAAGGATGACAAAGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTT 960
Db 901 CAAGGATGACAAAGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTT 960
Qy 961 CCTCTCAAACTCATCTTCTCAATGTCTGAACATGACTATGGGAACACTACCTTGC 1020
Db 961 CCTCTCAAACTCATCTTCTCAATGTCTGAACATGACTATGGGAACACTACCTTGC 1020
Qy 1021 GGCCTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGT 1080
Db 1021 GGCCTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGT 1080
Qy 1081 CAGCGAGTGCAGCAAGCGCAGCTCGAGGAGGCGAGCTGCTGCTGCTGCTCTTCT 1140
Db 1081 CAGCGAGTGCAGCAAGCGCAGCTCGAGGAGGCGAGCTGCTGCTGCTGCTCTTCT 1140
Qy 1141 GGTCTGCACTGCTCTCAATTTGATGTAGTGCCACTTCCCGACCGGGAAGGCT 1200
Db 1141 GGTCTGCACTGCTCTCAATTTGATGTAGTGCCACTTCCCGACCGGGAAGGCT 1200
Qy 1201 GCCGCCACCAACCAACCAACAGCAATGGCAACAGCAGCAAGCAACCAATCAGATA 1260
Db 1201 GCCGCCACCAACCAACCAACAGCAATGGCAACAGCAGCAAGCAACCAATCAGATA 1260
Qy 1261 TATCAAAATGAATTTAGAGAAACACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAC 1320
Db 1261 TATCAAAATGAATTTAGAGAAACACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAC 1320
Qy 1321 AAAGAATACCTTTGGGGGAAAGAGTTTAAAAAGAAATTCAGAAATGCTTGCAGATA 1380
Db 1321 AAAGAATACCTTTGGGGGAAAGAGTTTAAAAAGAAATTCAGAAATGCTTGCAGATA 1380
Qy 1381 TTTAGGTACAAATGGAGTTTCTTTCCCAACGGGAGGAGACACACACCCCGCTTGA 1440
Db 1381 TTTAGGTACAAATGGAGTTTCTTTCCCAACGGGAGGAGGAGACACACACCCCGCTTGA 1440
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RESULT 10

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ACA04211
ID ACA04211 standard; cDNA; 1679 BP.
XX
AC ACA04211;
XX
DT 27-MAY-2003 (first entry)
XX
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defects; premature aging; AIDS; biosensor;
acquired immunodeficiency syndrome; cancer; diabetic complication;
bioreactor; tumour
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-0137865.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 20-NOV-1998; 98WO-US24853.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
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PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31374.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US20116.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0815744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 18-JUL-2001; 2001US-0887879.
 PR 21-JUN-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 PR XX

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
 XX WPI; 2003-331925/31.
 DR P-PSDB; ABU67033.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer
 XX
 PS Claim 2; Fig 375; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear, utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIF,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence encodes a PRO protein of the invention.
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0% Score 1679; DB 25; Length 1679;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GTTGTCTCTTCAGCAACAGTGGATTAAATCTCTTCGACAGCTTGAGACACAC 60
 DB 1 GTTGTCTCTTCAGCAACAGTGGATTAAATCTCTTCGACAGCTTGAGACACAC 60
 OY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 OY 121 AAGAAAAAATCATGAAAAACCATCCAGCAAAATATCTATCTCTTGGGCAAT 180
 DB 121 AAGAAAAAATCATGAAAAACCATCCAGCAAAATATCTATCTCTTGGGCAAT 180
 OY 181 CTTTCAGGGGCTGGCTGCTGTCTCTTTCAAGAGTGCCTCGCGAGGAGATGC 240
 DB 181 CTTTCAGGGGCTGGCTGCTGTCTCTTTCAAGAGTGCCTCGCGAGGAGATGC 240
 OY 241 CACCTTCCCAAGCTATGACACACCTGACGCTCCCGGAGGAGAGAGAGAGAG 300
 DB 241 CACCTTCCCAAGCTATGACACACCTGACGCTCCCGGAGGAGAGAGAGAGAG 300
 OY 301 GTCCACTATGACACACGGGTGACCGGGTGCCTGCGCTAACCGGAGCACCCTCTA 360
 DB 301 GTCCACTATGACACACGGGTGACCGGGTGCCTGCGCTAACCGGAGCACCCTCTA 360

PR 09-SEP-1998; 98US-099601P.
 PR 10-SEP-1998; 98US-099803P.
 PR 10-SEP-1998; 98US-099811P.
 PR 10-SEP-1998; 98US-099812P.
 PR 17-SEP-1998; 98US-100858P.
 PR 24-SEP-1998; 98US-101922P.
 PR 28-OCT-1998; 98US-106032P.
 PR 20-NOV-1998; 98US-109304P.
 PR 23-MAR-1999; 99US-125778P.
 PR 15-JUN-1999; 99US-139695P.
 PR 20-JUL-1999; 99US-145070P.
 PR 26-JUL-1999; 99US-145698P.
 PR 17-AUG-1999; 99US-149396P.
 PR 07-DEC-1999; 99US-169495P.
 PR 15-NOV-2001; 2001US-0002796.
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy NA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX
 XX WPI: 2003-341964/32.
 DR P-PSDB; AB067293.
 XX
 XX Thirty seven nucleic acids encoding novel secreted and transmembrane
 PT PRO polypeptides, useful for modulating biological activity of cell
 PT expressing the polypeptide, and in chromosome and gene mapping
 XX
 XX Claim 2: Fig 51: 255pp; English.
 XX
 XX The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO333, PRO301, PRO187, PRO377, PRO1411, PRO10096, PRO246, PRO6307,
 CC factor receptor (FGR)-4, FGR-3, FGR-2 or FGR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (II) is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or
 CC anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
 CC diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency.
 CC disorders, for inhibiting tumour growth, enhances vascular permeability
 CC and immune response, for inducing regeneration of auditory hair cells and
 CC for treating hearing loss in mammals, and for treating bone and/or
 CC cartilage disorders such as sports injuries and arthritis. This sequence
 CC encodes a novel human secreted and transmembrane polypeptide
 CC associated oligonucleotide.
 XX
 XX Sequence 1679 BP: 498 A; 432 C; 419 G; 330 T; 0 other;
 Query Match 100.0%; Score 1679; DB 25; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GTGTGTCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAACAC 60
 Db 1 GTGTGTCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAACAC 60
 Oy 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 Db 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 Oy 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAATTTCTATCTCTTGGGCAAT 180
 Db 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAATTTCTATCTCTTGGGCAAT 180

121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAATTTCTATCTCTTGGGCAAT 180
 Oy 181 CTTACGCGGGCTGGCTGCTCTGTGTCTCTTCCAAAGAGTGCCTCGCGCAGCGAGATGC 240
 Db 181 CTTACGCGGGCTGGCTGCTCTGTGTCTCTTCCAAAGAGTGCCTCGCGCAGCGAGATGC 240
 Oy 241 CACCTTCCCAAAAGCTATGGAACAACGTGACGGTCCGGCAGGGGAGAGGCCACCTCAG 300
 Db 241 CACCTTCCCAAAAGCTATGGAACAACGTGACGGTCCGGCAGGGGAGAGGCCACCTCAG 300
 Oy 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCCTCTA 360
 Db 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCCTCTA 360
 Oy 361 TGTGGGAATGACAAGTGGTGGATCTCTCGCTGGTGGTCTCTGAGCAACACCAAC 420
 Db 361 TGTGGGAATGACAAGTGGTGGATCTCTCGCTGGTGGTCTCTGAGCAACACCAAC 420
 Oy 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
 Db 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
 Oy 481 GGTGCAGACAGAACCAACCAAGACCTCTAGGTGCTCAGCTCATTTGTGCAAGTATCTCC 540
 Db 481 GGTGCAGACAGAACCAACCAAGACCTCTAGGTGCTCAGCTCATTTGTGCAAGTATCTCC 540
 Oy 541 CAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAGGGGAACAATATTAGCTCAC 600
 Db 541 CAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAGGGGAACAATATTAGCTCAC 600
 Oy 601 CTCATACCACTGCTAGACAGAGCTTACGTTTACTTGGAGACACATCTCTCCAAAGC 660
 Db 601 CTCATACCACTGCTAGACAGAGCTTACGTTTACTTGGAGACACATCTCTCCAAAGC 660
 Oy 661 GGTGGCTTTGTGAGTGAAGCAATCTTTGGAATTTAGGGCATACACCGGAGAGTCT 720
 Db 661 GGTGGCTTTGTGAGTGAAGCAATCTTTGGAATTTAGGGCATACACCGGAGAGTCT 720
 Oy 721 AGGGGACTACGAGTGCCTCCCAATGACGTGGCGCGCCCTGTGTGCGAGAGATAA 780
 Db 721 AGGGGACTACGAGTGCCTCCCAATGACGTGGCGCGCCCTGTGTGCGAGAGATAA 780
 Oy 781 GGTACCGTGAATCTACACATACATTTTCAAGAGCCAAAGGTTACAGGTCTCCCGTGG 840
 Db 781 GGTACCGTGAATCTACACATACATTTTCAAGAGCCAAAGGTTACAGGTCTCCCGTGG 840
 Oy 841 ACAAAGGGGACACTGCAAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGT 900
 Db 841 ACAAAGGGGACACTGCAAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGT 900
 Oy 901 CAAGGATGACAAAGACTGTGTAAGAAAGAAAGGCTGAAAGTGGAAACAGACCTTT 960
 Db 901 CAAGGATGACAAAGACTGTGTAAGAAAGAAAGGCTGAAAGTGGAAACAGACCTTT 960
 Oy 961 CCTCTCAAACTCTCTCTCAATCTCTCTCAATCTCTCTCAATCTCTCTCAATCTCTCT 1020
 Db 961 CCTCTCAAACTCTCTCTCAATCTCTCTCAATCTCTCTCAATCTCTCTCAATCTCTCT 1020
 Oy 1021 GGCTCCAAAGCTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
 Db 1021 GGCTCCAAAGCTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
 Oy 1081 CAGCGAGGTGAGCAACAGCGACGTCGAGGAGGCGAGGCTGCGTCTGCGCTCTTCT 1140
 Db 1081 CAGCGAGGTGAGCAACAGCGACGTCGAGGAGGCGAGGCTGCGTCTGCGCTCTTCT 1140
 Oy 1141 GGTCTTGCACCTTCT 1200
 Db 1141 GGTCTTGCACCTTCT 1200
 Oy 1201 GCGCCACCCACCCACCAACAGCAATGGCAACACCGCAGCAACCAATCAGATA 1260
 Db 1201 GCGCCACCCACCCACCAACAGCAATGGCAACACCGCAGCAACCAATCAGATA 1260

QY 1261 TATCAAAATAGAAATAGAGAGAAACACAGCCTCATGAGCAGAGAAATTTGAGGAGGGGAAC 1320
Db 1261 TATCAAAATAGAAATAGAGAGAAACACAGCCTCATGAGCAGAGAAATTTGAGGAGGGGAAC 1320
QY 1321 AAAGAATACCTTTGGGGGAGAGAGTTTAAAAAGAGAAATTTGAAATTTGCTTGCAGATA 1380
Db 1321 AAAGAATACCTTTGGGGGAGAGAGTTTAAAAAGAGAAATTTGAAATTTGCTTGCAGATA 1380
QY 1381 TTTAGGTACAAATGGAGTTTCTTTTCCCAACCGGAGAAACACAGCAGACACCCGGCTTGA 1440
Db 1381 TTTAGGTACAAATGGAGTTTCTTTTCCCAACCGGAGAAACACAGCAGACACCCGGCTTGA 1440
QY 1441 CCCACTGCAAGCTGTCATGTCGCAACCTCTTTGCTGCGAGTGTGGCAAGGGCTCAGCCTC 1500
Db 1441 CCCACTGCAAGCTGTCATGTCGCAACCTCTTTGCTGCGAGTGTGGCAAGGGCTCAGCCTC 1500
QY 1501 TCTGCCACAGAGTGCCGCCACGTGGAACATCTGGAGCTGSCCATCCCAAAATTCATCA 1560
Db 1501 TCTGCCACAGAGTGCCGCCACGTGGAACATCTGGAGCTGSCCATCCCAAAATTCATCA 1560
QY 1561 GTCCATAGAGAGCAACAGANTGAGACCTTCGGGCCAAGCTGGCGTGGGGCAGCTTTG 1620
Db 1561 GTCCATAGAGAGCAACAGANTGAGACCTTCGGGCCAAGCTGGCGTGGGGCAGCTTTG 1620
QY 1621 GTAGCTGTCCACACACAGCGCTGTGTGTAACGTAATTAAGAGCAAAAAA 1679
Db 1621 GTAGCTGTCCACACACAGCGCTGTGTGTAACGTAATTAAGAGCAAAAAA 1679

RESULT 13

ABX89328
ID ABX89328 standard; cDNA; 1679 BP.

AC AC
XX ABX89328;

DT 13-MAY-2003 (first entry)
XX XX

DE DNA encoding novel secreted and transmembrane protein PRO337.
XX XX

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
XX cardiac insufficiency disorder; cancer; tumour; immune response;
XX adrenal cortical capillary endothelial growth; c-fos induction;
XX vascular endothelial growth factor inhibition; VEGF inhibition;
XX endothelial cell growth inhibitor; T-lymphocytes stimulation;
XX retinal neurons cell survival; rod photoreceptor cell survival;
XX retinal disorder; retinitis pigmentosa; kidney disorder;
XX mammalian kidney mesangial cell proliferation; Berger disease;
XX dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX chondrocyte redifferentiation; sports injury; arthritis; gene; ss.

OS Homo sapiens.
XX XX

XX US2003017563-A1.
XX XX

XX 23-JAN-2003.
XX XX

XX 07-MAY-2002; 2002US-0140808.
XX XX

XX 31-MAR-1997; 97WO-US05230.
XX 12-JUN-1998; 98WO-US12456.
XX 14-JUL-1998; 98WO-US14552.
XX 28-AUG-1998; 98WO-US17888.
XX 10-SEP-1998; 98WO-US18824.
XX 14-SEP-1998; 98WO-US19093.
XX 14-SEP-1998; 98WO-US19094.
XX 14-SEP-1998; 98WO-US19177.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 07-OCT-1998; 98WO-US21141.
XX 29-OCT-1998; 98WO-US22591.
XX 29-OCT-1998; 98WO-US22592.
XX 20-NOV-1998; 98WO-US24855.

PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28521.
PR 02-DEC-1999; 99WO-US28584.
PR 16-DEC-1999; 99WO-US28585.
PR 20-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 05-JAN-2000; 99WO-US31274.
PR 06-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0834280.
PR 18-MAY-2001; 2001US-0860216.

XX (GETH) GENENTECH INC.
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D,
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen WE,
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003:288163/28.
DR P-PSDB; AB061159.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies
XX
XX Claim 2: Fig 221: 459pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC The present sequence data for this patent was obtained in electronic
CC format directly from the USPRO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html.
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
Query Match 100.0%; Score 1679; DB 25; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 481 GGTGCAGACAGAAACACCAAGACCTCTTAGGTCCACCTCTTATGTGCAAGATATCTCC 540
Db 481 GGTGCAGACAGAAACACCAAGACCTCTTAGGTCCACCTCTTATGTGCAAGATATCTCC 540
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Db 541 CAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCCTCAC 600
Qy 601 CTGCATAGCAACTGGTACAGACAGAGCTTACGTTTACTTTGGAGACACATCTCTCCAAAGC 660
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Db 661 GTTTGGCTTTGTGAGTGAAGACGAATTTGGAATTTTCAAGGCAATCACCCGGGAGCAGTC 720
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RESULT 15
 ID AAZ47893
 XX AAZ47893 standard; cDNA; 1693 BP.
 AC AAZ47893;
 XX
 DT 10-MAR-2000 (first entry)
 XX
 DE Human protein encoding cDNA SEQ ID NO:3.
 XX
 KW Human; haematopoietic cell regulation; tissue generation; repair;
 KW activin; inhibitor; taxis; chemotaxis; blood coagulation; thrombus;
 KW receptor; ligand; autoimmune; infection-related immunodeficiency;
 KW inflammatory disorder; neurological disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FE CDS 214..1164
 FI /*tag= a
 XX
 PN WO958668-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 13-MAY-1999; 99WO-JP02485.
 XX
 PR 14-MAY-1999; 98JP-0131815.
 XX
 PA (ONOX) ONO PHARM CO LTD.
 XX
 PI Fukushima D, Shibayama S, Tada H;
 XX
 DR WPI; 2000-062298/05.
 DR P-PSDB; AAV57601.
 XX
 PT New polypeptides of human origin having cell regulatory, tissue:
 PT generation, coagulant and other activities
 XX
 PS Claim 5; Page 42-45; 84pp; Japanese.
 XX
 CC The present sequence encodes a specifically claimed novel human protein.
 CC The novel human protein can be used in therapeutic drugs for the
 CC prevention and treatment of a broad range of disorders including
 CC autoimmune and infection-related immunodeficiency, inflammatory
 CC disorders, and neurological diseases. The novel protein is expected of
 CC having haematopoietic cell regulatory activity, tissue generation/
 CC repair activity, activin/inhibin activity, taxis/chemotaxis activity,
 CC blood coagulation and thrombus activity, and receptor/ligand activity.
 XX
 SO Sequence 1693 BP; 518 A; 432 C; 416 G; 327 T; 0 other;

Query Match 99.0%; Score 1661.4; DB 21; Length 1693;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	343	20.4	1238	2	US-08-414-657D-3
2	343	20.4	1238	4	US-09-135-080-3
3	340.6	20.3	924	2	US-08-414-657D-7
4	340.6	20.3	977	2	US-08-414-657D-1
5	340.6	20.3	977	4	US-09-135-080-1
6	340.6	20.3	1014	2	US-08-414-657D-5
7	340.6	20.3	1014	4	US-09-135-080-7
8	338.6	20.2	861	2	US-08-414-657D-9
9	338.6	20.2	912	2	US-08-414-657D-6
10	337.4	20.1	945	2	US-08-414-657D-8
11	333.8	19.9	861	2	US-08-414-657D-10
12	303.6	18.1	756	2	US-08-414-657D-17
13	298.2	17.8	756	2	US-08-414-657D-18
14	100	6.0	219	2	US-08-414-657D-11
15	95.2	5.7	219	2	US-08-414-657D-12
16	77.8	4.6	177	2	US-08-414-657D-13
17	77.8	4.6	177	2	US-08-414-657D-14
18	65.6	3.9	198	2	US-08-414-657D-15
19	63.4	3.8	198	2	US-08-414-657D-16
20	50.2	3.0	2040	1	US-08-628-417-6
21	49.8	3.0	1048	4	US-09-489-847-38
22	48.6	2.9	1813	3	US-09-071-224-3
23	48.4	2.9	1117	3	US-09-247-373B-33
24	47.8	2.8	441	4	US-08-601-537-9
25	47.8	2.8	4121	4	US-09-601-537-9
26	47.6	2.8	2447	2	US-09-014-969-14
27	47.6	2.8	2674	4	US-09-817-180-1

28	47.4	2.8	1696	4	US-09-835-811-1	Sequence 1, Appl
29	46.8	2.8	2608	4	US-09-904-615-16	Sequence 16, Appl
30	46.6	2.8	569	4	US-09-461-325-44	Sequence 44, Appl
31	46.6	2.8	630	1	US-08-183-414E-1	Sequence 1, Appl
32	46.6	2.8	674	4	US-09-620-405B-465	Sequence 465, App
33	46.6	2.8	674	4	US-09-433-826B-465	Sequence 465, App
34	46.6	2.8	674	4	US-09-604-287A-465	Sequence 465, App
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36	46.6	2.8	1411	4	US-09-496-692-5	Sequence 5, Appl
37	46.6	2.8	1411	4	US-10-000-273-5	Sequence 5, Appl
38	46.6	2.8	2846	4	US-09-996-243-230	Sequence 230, App
39	46.6	2.8	3275	4	US-09-370-838-151	Sequence 151, App
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41	46.4	2.8	578	4	US-09-602-877A-95	Sequence 95, Appl
42	46.4	2.8	1020	4	US-09-328-475C-43	Sequence 43, Appl
43	46.4	2.8	2246	4	US-09-363-708-3	Sequence 3, Appl
44	46.4	2.8	2246	4	US-09-083-587-3	Sequence 3, Appl
45	46.4	2.8	2280	3	US-08-813-150-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Burea
; APPLICANT: Fischer, Izhak
; APPLICANT: Zikareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56...1069
; OTHER INFORMATION:
US-08-414-657D-3

Query Match 20.4%; Score 343; DB 2; Length 1238;
 Best Local Similarity 62.0%; Pred. No. 2,6e-80;
 Matches 598; Conservative 0; Mismatches 355; Indels 12; Gaps 3;

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 DB 121 TCTTCCACAGGAGTCCCGTGGCAGCGTGGAT-----TTTAAACCGAGCGACGAA 174

QY 265 GGTGACCGTCCGAGCGAGGAGCGCCACCTCAGGTGCACTATTGACAAACGGGTGAC 324
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QY 385 GGATCTCTCGGTGGTCTCTGAGCAACACCCAAAGCAGTACAGCATGATCCAGAA 444
 DB 295 GGACCTCTGGTGGAGCTGGAGAAAGCGCATGCTCTGGATACGCTCCGANTCCAGAA 354

QY 445 CGTGATGTGTATGACAGAGGGGCCCTTACACCTGCTCGGTGACAGACAGACACCA 504

RESULT 2
 US-09-135-080-3
 Sequence 3, Application US/09135080
 Patent No. 6433827
 GENERAL INFORMATION:
 APPLICANT: Levitt, Pat R.
 APPLICANT: Pimenta, Aurea
 APPLICANT: Fischer, Itzhak
 APPLICANT: Zhukareva, Victoria
 TITLE OF INVENTION: Limbic System-Associated Membrane
 TITLE OF INVENTION: Protein and DNA
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: decheit Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows, Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/135,080
 FILING DATE: 17-AUG-1998
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/414,657
 FILING DATE: 31-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-620-3214
 TELEFAX: 609-620-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1238 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 56..1069
 OTHER INFORMATION:
 US-09-135-080-3

Query Match 20.4%; Score 343; DB 4; Length 1238;
 Best Local Similarity 62.0%; Pred. No. 2,6e-80;
 Matches 598; Conservative 0; Mismatches 355; Indels 12; Gaps 3;

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QY 265 CGTGACCGTCCGAGCGAGGAGCGCCACCTCAGGTGCACTATTGACAAACGGGTGAC 324
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Db 355 GGTGGATGCTATGATGAAGGATCTACACATGCTCAGTTCAGACAGCATGAGCCAA 414
QY 505 GACCTCTAGGTCACCTCATTGTGAAGTATCTCCAAATTTAGAGATTTCTTCAGA 564
Db 415 GACCTCTCAAGTTTACTTGTACAGTTCACCAAGATCTCCAAATTTCTTCAGA 474
QY 565 TATCTCCATTAATGAAGGACATATTTAGCTTACCTGCTACAGTTCAGTTCAGTTCAG 624
Db 475 TGTCACTGTGAATGAGGACATATTTAGCTTACCTGCTACAGTTCAGTTCAGTTCAG 534
QY 625 GCTACGCTTACTTGGAGACATCTCTCCAAATTTAGCTTACCTGCTACAGTTCAGTTCAG 684
Db 535 ACTGTATACCTGAGACACCTTACACCTTGAAGAGATTTGAAGGAGAGAGAGA 594
QY 585 ATACTTGGAAATTCAGGATACCTCCGGGAGCAGTCAAGGAGTACAGTTCAGTTCAGTTCAG 744
Db 595 ATACTTGGAGATCTTGGACATCACAGGAGACAGTCAAGGAGTACAGTTCAGTTCAGTTCAG 654
QY 745 CAATGACGTGGCGCGCGGTGATGAGTAAAGTCAAGGATCAAGGATCAAGGATCAAGGATCA 804
Db 655 CAAGGAGTCTCTCCGGATGTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 714
QY 805 CATTTCAAGAGCAGGATGATGAGTAAAGTCAAGGATCAAGGATCAAGGATCAAGGATCAAG 864
Db 715 CATCAAGAGTCTTGAAGCAATGAAGCAAGTCAAGGATCAAGGATCAAGGATCAAGGATCA 774
QY 865 AGCTCAGCAGTCCCTCAGCAGATTTCCAGTGGTACAGGATGACAAAGGATCAAGGATCAAG 924
Db 775 AGCTCAGCAGTCCCTCAGCAGTCTTCAAGTGGTACAGGATGACAAAGGATCAAGGATCAAG 831
QY 925 AGAAAGAGAGGATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 984
Db 832 CAGTGAAGAGGATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 891
QY 985 TGTCTCTCAATGATGATGAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1044
Db 892 CGTCAAGAGGATGAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 951
QY 1045 CAATGACGATCATGCTATTTGCTCCAGGCGCTGACGAGTGAAGGATGACAAAGGATCAAG 1104
Db 952 CAATGACGATCATGCTATTTGCTCCAGGCGCTGACGAGTGAAGGATGACAAAGGATCAAG 1008
QY 1105 GAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
Db 1009 CAGTCTGGCGCTACCACTGTGGCTGTGGCAGCGTCCCTGTCTCTCAGCAAGTGA 1068
QY 1165 TTGAT 1169
Db 1069 TTGAT 1073

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RESULT 3
US-08-414-657D-7
Sequence 7, Application US/08414657D
Patent No. 5861283

GENERAL INFORMATION:

APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA

ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/414,657D
APPLICATION NUMBER: 5861283
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..924
OTHER INFORMATION:
US-08-414-657D-7

Query Match
Best Local Similarity: 63.3%; Score 340.6; DB 2; Length 924;
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

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QY 205 TCTCTCCAGGAGTCCCGTCCGAGCAGGAGATGCCACTTCCCAAGATATGGACAA 264
Db 45 TCTTCCACAGAGTCCCGTCCGAGCAGGAGTCCCGTCCCAAGATATGGACAA 98
QY 265 CGTACGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 324
Db 99 CATCACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 158
QY 325 CGGAGGCTGCTGCTAAACCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 384
Db 159 AAAGTGGCTGGTGAAGCCGTTCTGGGATCATTTTGGGATCATTTTGGGATCATTTTGGGAT 218
QY 385 GGATCTCTCGGCTGCTTCTGAGCAACACCCCAAGATCCAGATCCAGATCCAGATCCAGAT 444
Db 219 GGACCCACGAGGTTGAGCTGGAGAAACGCGCATTTCTTGGATATACAGCTCCGATCCAGAT 278
QY 445 CGTGGATGCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 504
Db 279 GGTGGATGCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 338
QY 505 GACCTCTAGGCTCCACCTCATTTGCAAGTATCTCCAAATTTAGAGATTTCTTCAGA 564
Db 339 GACCTCCCAAGTTTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 398
QY 565 TATCTCCATTAATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 624
Db 399 TGTCACTGTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 458
QY 625 GCTACGCTTACTTGGAGACATCTCTCCAAATTTAGCTTACCTGCTACAGTTCAGTTCAGTTCAG 684
Db 459 ACCTGTATCACTTGGAGACATCTTACCAATTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 518
QY 685 ATACTTGGAAATTCAGGATACCTCCGGGAGCAGTCAAGGATGACAAAGGATCAAGGATCAAG 744
Db 519 ATACTTGGAGATCTTGGACATCACAGGAGCAGTCAAGGATGACAAAGGATCAAGGATCAAG 578
QY 745 CAATGACGTGGCGCGCGGTGATGAGTAAAGTCAAGGATCAAGGATCAAGGATCAAGGATCAAG 804
Db 579 CAAGGAGTCTCTCCGGGATGAGTAAAGTCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 638

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TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1014
OTHER INFORMATION:
US-08-414-657D-5

Query Match 20.3%; Score 340.6; DB 2; Length 1014;
Best Local Similarity 61.9%; Pred. No. 1e-79;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;
QY 205 TCTCTTCCAGGAGTCCCGTCCGCGAGGAGATGCCACCTTCCCAAGCTATGACAA 264
DB 66 TCTTCCACAGGAGTCCCGTCCGCGAGGAGATGCCACCTTCCCAAGCTATGACAA 119
QY 265 CGTGACGGTCCCGGAGGAGGAGCGCCACCTTCCAGTGCATATTGACAAACGGGTAC 324
DB 120 CATCACGGTCCCGGAGGAGGAGCGCCACCTTCCAGTGCATATTGACAAACGGGTAC 179
QY 325 CGGGTGGCTGGCTAAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 384
DB 180 GAAAGTGGCTGGCTAAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 239
QY 385 GGATCTCGCGTGGCTTCTGAGCAACACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 444
DB 240 GGACCTCGCGTGGCTTCTGAGCAACACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 299
QY 445 CGTGATGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 504
DB 300 GGTGATGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 359
QY 505 GACCTCTAGGCTTCTGAGCAACCTTCTGAGCAACCTTCTGAGCAACCTTCTGAGCAAC 564
DB 360 GACCTCTAGGCTTCTGAGCAACCTTCTGAGCAACCTTCTGAGCAACCTTCTGAGCAAC 419
QY 565 TATCTCATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 624
DB 420 TGTACTGTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 479
QY 625 CCTACGGTTACTTGGAGACACATCTCTCCCAAGCGTGGCTTGTGAGTGAAGAGCA 684
DB 480 ACCTGTATCCTTGAGACACATCTCTCCCAAGCGTGGCTTGTGAGTGAAGAGCA 539
QY 685 ATACTTGAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 744
DB 540 ATACTTGAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 599
QY 745 CAATGAGTGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 804
DB 600 CAAGGAGGCTCTCTCGGCGGATGTCAACCAAGTCAAGGCTCACTGTGAACCTATCCACCC 659
QY 805 CATTTGAGAGGCAAGGAGTACAGGTGTCCCGTGGGAGCAAAAGGGGAGACCTGAGTGTGA 864
DB 660 CATCACAGAGTCTAAGAGCAATGAAGCCACACAGGAGCAACGCTTCCCTCAATGTGA 719
QY 865 AGCCTCAGAGTCCCTCAGCAGAAATTCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 924
DB 720 AGCCTCAGAGTCCCTCAGCAGAAATTCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 776
QY 925 AGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 984
DB 777 CAGTGCAGAGGCTTGAGATTAGACCACTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 836
QY 985 TGTCTGTGACATGACTATGGAACCTACTTCCGTGGCTTCCAGAGCTGGGCGGAGCAAC 1044
DB 837 CGTCACTGAGGAACACTAGGCAACTATACCTGTGTGGCTGCCAAGCAAGCTCGGGGTAC 896

QY 1045 CAATCCAGCATCATGCTATTGGTCCAGGCGCGTCCAGGAGGAGGAGGAGGAGGAGGAGG 1104
DB 897 CAATCCAGCATCATGCTATTGGTCCAGGCGCGTCCAGGAGGAGGAGGAGGAGGAGGAGG 953
QY 1105 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1164
DB 954 CAGTGTGCCCTACCACTGTGCTGCTGCGAGCGCTCCTCTTCTGCTTCTCAGCAATG 1013
QY 1165 T 1165
DB 1014 T 1014

RESULT 7
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
; US-09-135-080-7

Query Match 20.3%; Score 340.6; DB 4; Length 1014;
Best Local Similarity 61.9%; Pred. No. 1e-79;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;
QY 205 TCTCTTCCAGGAGTCCCGTCCGCGAGGAGATGCCACCTTCCCAAGCTATGACAA 264
DB 66 TCTTCCACAGGAGTCCCGTCCGCGAGGAGATGCCACCTTCCCAAGCTATGACAA 119
QY 265 CGTGACGGTCCCGGAGGAGGAGCGCCACCTCAGTGCATATTGACAAACGGGTAC 324


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QY 673 GAGTGAAGACGAATCTTGGAAATTCAGGCGCATCACCGGAGCAGTCAGGGACTACGA 732
DB 444 AGGAGAAGAAGATATCTGGAGATCTTGGCATCACCGAGGAGCAGTCAGCAATATGA 503
QY 733 GTGCAAGTCTCCAAATGACGTGCGCGCCGCTGGTACGGAGAGTAAAGTTCACCGTGA 792
DB 504 GTGCAAGTCTCCAAATGACGTGCGCGCCGCTGGTACGGAGAGTAAAGTTCACCGTGA 563
QY 793 CTATCCACCATACATTTGAGAGCCAGGGTACAGGTGTCCTCCGTCGCAAAAGGGGAC 852
DB 564 CTATCCACCATACATTTGAGAGCCAGGGTACAGGTGTCCTCCGTCGCAAAAGGGGAC 623
QY 853 ACTGCAAGTGAAGCCTCAGCAGTCCCTCAGCAGAGTAAAGTTCAGGTGACAGGATGACA 912
DB 624 ACTCAATGTGAGGCTCGGCGCTGCTGACCTGACCTTGGTGGTACCGGAGTACGAC 683
QY 913 AAGACTGATGAAGAAAGAGGGGTGAAGTGGGAAAGACAGACCTTCTCTCAAAACT 972
DB 684 TAG---GATAAATAGTCCAAATGGCTTGAGATTAGAGCAGCGGAGGGCGAGTTCCT 740
QY 973 CATCTCTTCAATGTCTGAAACATGACTATGGGAACTACACTTGGGTGCGCTCCCAACA 1032
DB 741 GACGGTGACCAAGCTGACTGAGGAGCACTACCGCAACTACACCTGTGTGGCTGCCAACA 800
QY 1033 GCTGGGCGCACCAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCG 1085
DB 801 GCTGGGCGTCACCAATGCCAGCTAGTCTCTTTTCAGACCTGGGTGCGTGAGAG 853

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RESULT 9

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US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF INVENTIONS: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..912
; OTHER INFORMATION:
US-08-414-657D-6

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Query Match

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Best Local Similarity : 63.7%; Pred. No. 3.2e-79;
Matches 531; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
20.2%; Score 338.6; DB 2; Length 912;
QY 253 ACCTATGACAAACGTGACGGTCCGGCAGGGAGAGCGCCACCTCAGGTGCACTATTGA 312
DB 24 AGGCAGGACAAACATCACCCTGAGGCGAGGGGACACAGCATCTCTCAGGTGCGTCTAGA 83
QY 313 CAACCGGTGACCCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA 372
DB 84 AGACAAGAACTCAAAAGGTGGCTGCTGACCGCTTCTGGCATCATTTTCTGGGACATGA 143
QY 373 CAAGTGTGCTGATCTCTGCGGTGGTCTTCTGAGCAACACCCAAACGCAAGTACAGCAT 432
DB 144 CAAGTGTGCTGATCTCTGACCGCGGTGAGCTGGAGAAACGCAATCTCTGGGAATACAGCCT 203
QY 433 CGAGATCCAGAAAGCTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCGACAGAGA 492
DB 204 CGAATCCAGAAAGTGGATGCTATGATGAGGGTTCCTACACCTGCTCAGTTTCAGACACA 263
QY 493 CAACCAACCAAGACCTCTAGGCTCCACCTCATTTGTGAGATATCTCCCAAAATTTAGA 552
DB 264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGTATGATGATGATGATGATGATGATGAT 323
QY 553 GATTTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCAGCTCAGTACGAA 612
DB 324 TATCTCTCGGATGTCATGTGATGAGGCGCAACGCTGACTGTGCTGCTGCTGCTGCTGCT 383
QY 613 TGTAGACGACGAGCTACGGTTACTTTGAGACACATCTCCCAAGAGGGTGTGCTTGT 672
DB 384 TGGCGTCTGTAACCTGTTATCACCTGCGAGACACCTTTACACCAACTGGAAGGAATTTGA 443
QY 673 GAGTGAAGACGAATCTTGGAAATTCAGGCGCATCACCGGAGCAGTCAGGGACTACGA 732
DB 444 AGGAGAAGAAGATATCTGGAGATCTTGGCATCACCGAGGAGCAGTCAGCAATATGA 503
QY 733 GTGCAAGTCTCCAAATGACGTGCGCGCCGCTGGTACGGAGAGTAAAGTTCACCGTGA 792
DB 504 GTGCAAGTCTCCAAATGACGTGCGCGCCGCTGGTACGGAGAGTAAAGTTCACCGTGA 563
QY 793 CTATCCACCATACATTTGAGAGCCAGGGTACAGGTGTCCTCCGTCGCAAAAGGGGAC 852
DB 564 CTATCCACCATACATTTGAGAGCCAGGGTACAGGTGTCCTCCGTCGCAAAAGGGGAC 623
QY 853 ACTGCAAGTGAAGCCTCAGCAGTCCCTCAGCAGAGTAAAGTTCAGGTGACAGGATGACA 912
DB 624 ACTCAATGTGAGGCTCGGCGCTGCTGACCTGACCTTGGTGGTACCGGAGTACGAC 683
QY 913 AAGACTGATGAAGAAAGAGGGGTGAAGTGGGAAAGACAGACCTTCTCTCAAAACT 972
DB 684 TAG---GATAAATAGTCCAAATGGCTTGAGATTAGAGCAGCGGAGGGCGAGTTCCT 740
QY 973 CATCTCTTCAATGTCTGAAACATGACTATGGGAACTACACTTGGGTGCGCTCCCAACA 1032
DB 741 GACGGTGACCAAGCTGACTGAGGAGCACTACCGCAACTACACCTGTGTGGCTGCCAACA 800
QY 1033 GCTGGGCGCACCAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCG 1085
DB 801 GCTGGGCGTCACCAATGCCAGCTAGTCTCTTTTCAGACCTGGGTGCGTGAGAG 853

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RESULT 10

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US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283

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REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..861
OTHER INFORMATION:
US-08-414-657D-10

Query Match 19.9%; Score 333.8; DB 2; Length 861;
Best Local Similarity 63.4%; Pred. No. 5.6e-78;
Matches 528; Conservative 0; Mismatches 302; Indels 3; Gaps 1;
QY 253 AGCTATGGACAAACGTCACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGA 312
DB 24 AGGCACGACAAACATCACCCTGAGGCAGGGGAGAGCGCCATCCTCAGGTGTGTGTAGA 83
QY 313 CAACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCACCTCTCTATCTGGGAATGA 372
DB 84 AGACAAGAACTCGAAAGTGGCTGTGTGAACCGCTCTGTCATCATCTTCGCTGGACAGA 143
QY 373 CAAGTGTGGTGGATCTCGCTGGTCTCTGACACACACCCAAACGACGTACAGCAT 432
DB 144 CAAGTGTCTGGACCTCGGGTTGAGCTGGGAAACGCCATCTCTGGAATACAGCT 203
QY 433 CGAGATCCAGACGTGGATGTATGAGAGAGGCCCTTACACCTGCTGCTGGTGCAGACAGA 492
DB 204 CGAATCCAGAGGTGGATGTATGATGAAGATCTTACACATCTGCTGCTGACAGACA 263
QY 493 CAACACCCAAAGACCTTAGGGTCCACCTCATTTGGAAGTATCTCCCAAAATGTAGA 552
DB 264 GCATGAGCCCAAGACCTCTCAAGTTTACTTGTATGTATGATGTACCAAGATCTCCAA 323
QY 553 GATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCACCTGCATAGCAAC 612
DB 324 CATCTCTCGATGTCACTGTGAATGAGGCGACAAATGTAACCTGTGTGCTGATGCCAA 383
QY 613 TGGTAGACAGACCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGTGTGGCTTTGT 672
DB 384 TGGCGCCCTGAACCTGTATACCTTGGAGACACCTTACACCACTTGGAAAGAAATTTGA 443
QY 673 CAGTGAAGACGAATCTTGGAAATTCAGGACATCACCGGGAGCAGTCAGGGGACTAGA 732
DB 444 AGGAGAAGAAATATCTGGAGATCTTAGCATCACAGGGAACAGTCAGGCAAAATATGA 503
QY 733 GTGCAGTGTCCCAATGAGCTGGCGGCCGCTGTTGAGAGAGTAAAGTCAAGCTGAA 792
DB 504 GTGCAAGCTGCCACAGAGTCTCTCCGGGATGTCAACAAGTCAAGTCACTGTGNA 563
QY 793 CTATCCACCATATCTTCAAGCCAGGTACAGTGTCCCGTGGGACAAAGGGGAC 852
DB 564 CTATCCACCATATCTTCAAGCCAGGTCTAAGCAATTAAGCCACACAGAGGACGAGCTTC 623
QY 853 ACTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGGTACAAAGGATGACAA 912
DB 624 CCTCAATGTGAAGCCTCAGGCGGTGCTGCACCTGACTTTGAGTGGTACCGGATGACAC 683
QY 913 AAGACTGATTGAAGGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAACT 972
DB 684 CAG---GATAAACAGTGAACAGCGCTTGAGATTGAAGACACTGAGGGCCAGTCTCCCT 740
QY 973 CATCTCTTCAATGTCTTGAACATGATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1032
DB 741 GACGGTGACCAACGCTACTGAGGACACTACGCAACTATACCTGTGTGCTGCCAACNA 800

QY 1033 GCTGGGACACACCAATGCCAGCATCATCTATTGTTGGTCCAGGCGGCTCAGCG 1085
DB 801 GCTGGGCTCACCATGCCAGCATCTAGTCTCTTTTCAGACCCGCGTGGTGAG 853
RESULT 12
US-08-414-657D-17
Sequence 17, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..756
OTHER INFORMATION:
US-08-414-657D-17

Query Match 18.1%; Score 303.6; DB 2; Length 756;
Best Local Similarity 63.5%; Pred. No. 4.4e-70;
Matches 461; Conservative 0; Mismatches 274; Indels 3; Gaps 1;
QY 281 GGGGAGAGCGCCACCTCTAGGTGCACTATTGACAAACCGGTTCACCGGGTGGCTGGCTA 340
DB 1 GGGGACAGAGCATCTCTAGGTGCGCTCTAGAAGACAAAGAACTCAAAGGTGGCTGGTTG 60
QY 341 AACCCGACAGCATCTCTATGCTGGGAATGACAAGTGGTCCCTGATCTCTGGCTGGTC 400
DB 61 AACCTTCTGGCATATTTTGTGTCATGACATGCAAGTGGTCTCTGGACCCAGCGGTGAG 120
QY 401 CTCTCTGACCAACCCCAACGAGCAGTACAGCATCCAGATCCAGAACTGATGTGTATGAC 460
DB 121 CTGGAGAAACCCATCTCTGGAATACAGCTCCGAATCCAGAAAGTGGATGTCTATGAT 180
QY 461 GAGGCCCCCTTACACTCTCTGCTGGTGGCAGACAGACAAACCCCAAGACCTCTAGGTCCAC 520

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181 GAGGGTCTTACACTGCTCAGTTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTAC 240
521 CTCATTGTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAA 580
241 TTGATCGTACAAAGTCCCAACCAAGATCTCCAATATCTCTCGGATGCTCACTGATGAC 300
581 GCGAACAATATTAGCTTCACTGCTAGCACTGCTAGCACTGCTAGCACTGCTAGCTGCTAG 640
301 GCGAGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
641 AGACATCTCTCCCAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
361 AGACATCTTACCACTGGAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
701 GCGATCAGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
421 GCGATCAGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
761 CCGGTGCTAGGAGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
481 GCGATGCTCAACAGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
821 GGTACAGTGTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
541 AGCAATGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
881 TCAGCAATTCAGTGTACAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 940
601 GCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
941 AAGTGGAAACAGACCTTCTCTCCAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
658 GAGATTAAGACGACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
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RESULT 13
US-08-414-657D-18
; Sequence 18, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Lmbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen

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REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...756
OTHER INFORMATION:
US-08-414-657D-18

Query Match 17.8%; Score 298.2; DB 2; Length 756;
Best Local Similarity 53.0%; Pred. No. 1.2e-68;
Matches 478; Conservative 0; Mismatches 278; Indels 3; Gaps 1;

Qy 281 GGGGAGAGCGCCACCCTCAGGTGACATATTGACAACGGGTGTCACCCGGGTGGCTGCTA 340
Db 1 GGGGAGAGCGCCACCCTCAGGTGACATATTGACAACGGGTGTCACCCGGGTGGCTGCTA 60
Qy 341 AACCGCAGCACCCTCCTCTATGCTGGGAATGACAAGTGGTGGCTGCTGCTGCTGCTGCT 400
Db 61 AACCGCAGCACCCTCCTCTATGCTGGGAATGACAAGTGGTGGCTGCTGCTGCTGCTGCT 120
Qy 401 CTTCTGAGCAACACCCAAACGAGTACAGATCGAGATCCAGAACGAGTGGTCTCTGGACC 460
Db 121 CTTGAGAAACGACCTCTCTGGAATACAGCTCGGAATCCAGAACGAGTGGTCTCTGGACC 180
Qy 461 GAGGCGCTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 520
Db 181 GAGGCGCTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 521 CTCATTGTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAA 580
Db 241 TTGATTGTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAA 300
Qy 581 GGGACAAATATTAGCTCCTCAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 640
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Qy 701 GCGATCAGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
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Qy 761 CCGGTGCTAGGAGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820
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RESULT 14
US-08-414-657D-11
Sequence 11, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..219
OTHER INFORMATION:
US-08-414-657D-11

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Best Local Similarity 67.0%; Pred. No. 6.3e-17;
Matches 142; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
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QY 341 ACCCGAGCAGCACCCTCTATGCTGGGATGACAGTGGTCCCTGGATCTCGCGTGGTC 400
DB 61 ACCCGTCTGGCATCATTTTGGTGGCATGACAAAGTGGTCTCTGACCCCGGGTTGAG 120
QY 401 CTCTGTGAGCAACCCAAAGCCAGTACAGATCGAGATCCAGACGTTGGATGTGTATGAC 460
DB 121 CTGGAGAAAGCCGATCTCTGGATATACAGCTCCGAATCCAGAAAGTGGATGTCTATGAT 180
QY 461 GAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
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RESULT 15
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Sequence 12, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..219
OTHER INFORMATION:
US-08-414-657D-12

Query Match 5.7%; Score 95.2; DB 2; Length 219;
Best Local Similarity 65.6%; Pred. No. 1.1e-15;
Matches 139; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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DB 1 GGGGACACAGCCATCCACGGTGGTCTTAGAAGACAGAACTCAAGTGGCGCTGGTG 60
QY 341 ACCCGAGCAGCACCCTCTCTATGCTGGGATGACAGTGGTCCCTGGATCTCGCGTGGTC 400
DB 61 ACCCGTCTGGCATCATTTTGGTGGCATGACAAAGTGGTCTCTGACCCCGGGTTGAG 120
QY 401 CTCTGTGAGCAACCCAAAGCCAGTACAGATCGAGATCCAGACGTTGGATGTGTATGAC 460
DB 121 CTGGAGAAAGCCGATCTCTGGATATACAGCTCCGAATCCAGAAAGTGGATGTCTATGAT 180
QY 461 GAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
DB 181 GAGGATCTTACACATGCTCTAGTTCAGACACA 212

Thu Sep 11 16:20:48 2003

us-10-017-084a-522.rni

Page 13

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Job time : 157 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
7176.413 Million cell updates/sec

Title: US-10-017-084a-522
Perfect score: 1679
Sequence: 1 gttgtctcttcgcaaac.....ataaaagagcaaaaaa 1679

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues 3264840
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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6	1679	100.0	1679	11	US-09-978-608A-522 Sequence 522, App
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25	1679	100.0	1679	12	US-10-140-018-375 Sequence 375, App
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29	1679	100.0	1679	12	US-10-140-807-375 Sequence 375, App
30	1679	100.0	1679	12	US-10-140-922-375 Sequence 375, App
31	1679	100.0	1679	12	US-10-140-924-375 Sequence 375, App
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33	1679	100.0	1679	12	US-10-141-698-375 Sequence 375, App
34	1679	100.0	1679	12	US-10-141-702-375 Sequence 375, App
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ALIGNMENTS

RESULT 1
US-09-978-295A-522
Sequence 522, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Iivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30

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 3 PRIOR APPLICATION NUMBER: 60/064249
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 6 PRIOR FILING DATE: 1997-11-13
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 8 PRIOR FILING DATE: 1997-11-21
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DB	61	ATCTATATAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120						
QY	121	AGAAAGAAATCATGAAACCATCCAGCCAAAGAAATGCACAAATTTCTCTCTGGGCAAT	180						
DB	121	AGAAAGAAATCATGAAACCATCCAGCCAAAGAAATGCACAAATTTCTCTCTGGGCAAT	180						
QY	181	CTTACGGGGCTGGCTGTCTGTCTCTCTTCCAAAGAGTGGCTGCGGAGGAGGATGC	240						
DB	181	CTTACGGGGCTGGCTGTCTGTCTCTTCCAAAGAGTGGCTGCGGAGGAGGATGC	240						
QY	241	CACCTTCCCAAGCATATGACAACTGACGGTCCGGGAGGAGGAGGAGGAGGAGGAG	300						
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QY	301	GTGCACTATTGACAAACCGGGTCCCGGGTGGCTGCTAAACCGGAGGAGGAGGAGGAG	360						
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QY	361	TGCTGGGAATGACAAGTGGTGGCTGGATCTCGCTGGTCTCTCTGAGCAACACCAAC	420						
DB	361	TGCTGGGAATGACAAGTGGTGGTGGATCTCTCGCTGGTCTCTCTGAGCAACACCAAC	420						
QY	421	GCAGTACAGCATCGAGATCCAGACGTTGATGATGATGATGATGATGATGATGATGAT	480						
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QY	481	GGTGCAGACAGAC	540						
DB	481	GGTGCAGACAGAC	540						
QY	541	CAAAATTTAGAGATTTCTCAGATATCTCCATTAATGAAGGGAACAAATATAGGCTCAC	600						
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QY	601	CTGCATAGCACTGGTAGACACAGAGCTTACGGTTACTTTGGAGACACATCTCTCCAAAGC	660						
DB	601	CTGCATAGCACTGGTAGACACAGAGCTTACGGTTACTTTGGAGACACATCTCTCCAAAGC	660						
QY	661	GGTTGGCTTTGTGAGTGAAGCAACTTGGAAATTCAGGGATCACCGGGGAGCAGTC	720						
DB	661	GGTTGGCTTTGTGAGTGAAGCAACTTGGAAATTCAGGGATCACCGGGGAGCAGTC	720						
QY	721	AGGGGACTACGAGTGCAGTGCCTCCCAATGACCTGCGCGCGCGCTGACGGAGATGAA	780						
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RESULT 2
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 ; Sequence 522, Application US/09978697
 ; Patent No. US20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrarini, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlsen, Mary E.
APPLICANT: Godard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavrin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
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7	PRIOR APPLICATION NUMBER: 60/084414	421	GCAGTACAGCATCGAGATCCAGAACGTGATGTATGACGAGGGCCCTTACACCTGCTC	480
8	PRIOR FILING DATE: 1998-05-06	481		
9	PRIOR APPLICATION NUMBER: 60/084441	481	GGTGACAGACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	540
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11	PRIOR APPLICATION NUMBER: 60/084637	481	GGTGACAGACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	540
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13	PRIOR APPLICATION NUMBER: 60/084639	541	CAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAACAATATATAGCTCAC	600
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15	PRIOR APPLICATION NUMBER: 60/084640	601	CTGCATAGCAACTGGTAGACAGAGCTACGCTTACTTTGGAGACATCTCTCCCAAGC	660
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17	PRIOR APPLICATION NUMBER: 60/084598	601	CTGCATAGCAACTGGTAGACAGAGCTACGCTTACTTTGGAGACATCTCTCCCAAGC	660
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19	PRIOR APPLICATION NUMBER: 60/084600	661	GCTTGGCTTTGTGAGTGAAGACGAAATCTTGAATTTAGGCGATCCCGGAGCAGTC	720
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21	PRIOR APPLICATION NUMBER: 60/084627	661	GCTTGGCTTTGTGAGTGAAGACGAAATCTTGAATTTAGGCGATCCCGGAGCAGTC	720
22	PRIOR FILING DATE: 1998-05-07	721		
23	PRIOR APPLICATION NUMBER: 60/084643	721	AGGAGCTACAGTGCAGTGCCTCCANTGACGTGGCGCCCGCTGACGAGAGTAA	780
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25	PRIOR APPLICATION NUMBER: 60/085339	721	AGGAGCTACAGTGCAGTGCCTCCANTGACGTGGCGCCCGCTGACGAGAGTAA	780
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33	PRIOR APPLICATION NUMBER: 60/085700	841	ACAAAGGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGT	900
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35	PRIOR APPLICATION NUMBER: 60/085689	901	CAAGATGACAAAAGACTGATTTGAAGAAAGAAAGGGTGAAGTGAAGAAACAGACCTT	960
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37	PRIOR APPLICATION NUMBER: 60/085579	901	CAAGATGACAAAAGACTGATTTGAAGAAAGAAAGGGTGAAGTGAAGAAACAGACCTT	960
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47	PRIOR APPLICATION NUMBER: 60/085579	1081	CAGCAGGTGAGCAACGGCAGCTGCGAGGAGGCGAGCTGGCTGGCTGGCTGGCTGGCT	1140
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QY	61	AACTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120	
DB	61	AACTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120	
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DB	121	AGAAAGAAATCATGAAACCAATCCAGCCAAATGACAAATTTCTATCTTTGGGCAAT	180	
QY	181	CTTCAGGGGCTGGCTGCTGTGCTCTTCTTCCAAAGGAGTGGCCGTGGCAGGAGATGC	240	
DB	181	CTTCAGGGGCTGGCTGCTGTGCTCTTCTTCCAAAGGAGTGGCCGTGGCAGGAGATGC	240	
QY	241	CACCTTCCCAAGCTATGGACAGGTGACGTGCGCAGGGGAGAGGCGCCACCTCAG	300	
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Dd	1501	TCTGCCCCACAGAGTGCCCCCACCTGGGAACATTCTGGAGCTGGGCCATCCCAAATTAACAATCA	1560
Oy	1561	GTCATATAGAGACGAACAGAATGAGACTTCCTGGGCCCAAGCGTGGCGCTCGCGGCACACTTG	1620
Dd	1561	GTCATATAGAGACGAACAGAATGAGACTTCCTGGGCCCAAGCGTGGCGCTCGCGGCACACTTG	1620
Oy	1621	GTAGACTGTGCCACACGCGCGCTGTGTGTGAAGCTGAAATAAAAAAGACAAAAA	1679
Dd	1621	GTAGACTGTGCCACACGCGCGCTGTGTGTGAAGCTGAAATAAAAAAGACAAAAA	1679

RESULT 3

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US-97-978-192A-522
: Sequence 532, Application US/09978192A
: Patent No. US2002017753A1
GENERAL INFORMATION:
: APPLICANT: ASHKENAZI, Avl
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Besnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Trans
: TITLE OF INVENTION: Acids Encoding th
: FILE REFERENCE: P7630P1C9
CURRENT APPLICATION NUMBER: US/09/978-
CURRENT FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 09/918585
PRIORITY FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/064249
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PRIORITY APPLICATION NUMBER: 60/077641
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PRIORITY APPLICATION NUMBER: 60/077649
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Query Match	100.0%;	Score 1679;	DB 10;	Length 1679;
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Db	61	AATCTATCAGGAAAGAAAGAAAAAACCCGAAACCTGCACAAAAAGAAAGAAAAAG	120	
Qy	121	AAGAAAAAATCATGAAACCATTCCAGCCCAAAATGCAAAATCTATCTCTTTGGCAAT	180	
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Qy	181	CTTCACGGGCTGGTGTCTGTCTCTCTCTCTTCCAAAGAGTGGCCGTGCGCAGCGAGATGC	240	
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Qy	241	CACCTTCCCCAAAGTATGGAACAACGTGACGGTCCGGCAGGGGAGAGCCCAACCTCAG	300	
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Qy	301	GTGCACATATTGACAACCCGGGTACCCGGGTGGCGTGGCTAAACCGCAGCACCATCTCTTA	360	
Db	301	GTGCACATATTGACAACCCGGGTACCCGGGTGGCGTGGCTAAACCGCAGCACCATCTCTTA	360	
Qy	361	TGCTGGGAATGACAAAGTGGTGGCTGGGATCCCTGGCTGGTCTCTTGAGCAACCAAC	420	
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Qy	421	CGAGTACAGCATCGAGATCCAGAACGTGAGTGTGTATGACGAGGGCCCTTACACGTGTC	480	
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Db	541	CAAAATTTGATAGATTTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600	
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Db	601	CTGCATAGCAACTGTTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGC	660	
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Db	661	GGTTGGCTTTGTGAGTGAAGACGAATACTTTGGAATTCAGGGCATCACCCGGGAGCAGTC	720	
Qy	721	AGGGGACTACGAGTGCAGTCCCTCCAATGACGTGGCGCGCCGTGTGTCGGAGAGTAAA	780	
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Qy	781	GGTCACCGTGAACATATCCACCATACATTTTCAGACCAAGGTACAGTGTCTCCCGTGG	840	
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Qy	841	ACAAAGGGGACACTGAGGTGTGAGCCTCAGCATGCCCTTCAGCAGAAATTCAGTGTA	900	
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;; PRIOR FILING DATE: 1998-04-09
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;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081955
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081817
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081952
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;; PRIOR APPLICATION NUMBER: 60/083322
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;; PRIOR APPLICATION NUMBER: 60/083495
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;; PRIOR APPLICATION NUMBER: 60/083496
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;; PRIOR APPLICATION NUMBER: 60/084598

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;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 1679; DB 10; Length 1679;

Best Local Similarity 100.0% Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	Db	1	GTGTGTCCTTCAGCAAAACAGTGGATTAATCTCTCTGACAAAGCTTGAGACACAC	60
Qy	Db	1	GTGTGTCCTTCAGCAAAACAGTGGATTAATCTCTCTGACAAAGCTTGAGACACAC <th>60</th>	60
Qy	Db	61	AATCTATCAGCAAGAAAGAAAGAAACCGCAACCTGACAAAAGAAAGAAAGAAAG <th>120</th>	120
Qy	Db	61	AATCTATCAGCAAGAAAGAAAGAAACCGCAACCTGACAAAAGAAAGAAAGAAAG <th>120</th>	120
Qy	Db	121	AAGAAAAAATCATGAAACCATCCAGCCAAATATCTATCTCTTGGGCAAT <th>180</th>	180
Qy	Db	121	AAGAAAAAATCATGAAACCATCCAGCCAAATATCTATCTCTTGGGCAAT <th>180</th>	180
Qy	Db	181	CTTCACGGGGCTGGCTCTCTGTCTCTTCCAAAGAGTGGCCGTCGCGAGGAGATGC <th>240</th>	240
Qy	Db	181	CTTCACGGGGCTGGCTCTCTGTCTCTTCCAAAGAGTGGCCGTCGCGAGGAGATGC <th>240</th>	240
Qy	Db	241	CACCTTCCCAAAAGCTATGGCAACGTGACCGGTCCGCGAGGGGAGAGCCACCTTCAG <th>300</th>	300
Qy	Db	241	CACCTTCCCAAAAGCTATGGCAACGTGACCGGTCCGCGAGGGGAGAGCCACCTTCAG <th>300</th>	300
Qy	Db	301	GTGCACATATTGACAAACCGGTGTCACCGGGTGGCTGCTAAACCCGACGACCACTCTCTA <th>360</th>	360
Qy	Db	301	GTGCACATATTGACAAACCGGTGTCACCGGGTGGCTGCTAAACCCGACGACCACTCTCTA <th>360</th>	360
Qy	Db	361	TCCTGGGAATGCAAGTGGTGGATCTCTCGGTGGTCTCTTCTGACGACACCCAAAC <th>420</th>	420
Qy	Db	361	TCCTGGGAATGCAAGTGGTGGATCTCTCGGTGGTCTCTTCTGACGACACCCAAAC <th>420</th>	420
Qy	Db	421	GCATACAGCATCGAGATCCAGACGTGGATGTGTATGACGAGGGCCCTTACCTGCTC <th>480</th>	480
Qy	Db	421	GCATACAGCATCGAGATCCAGACGTGGATGTGTATGACGAGGGCCCTTACCTGCTC <th>480</th>	480
Qy	Db	481	GTGACAGACAGAACCCCAAGAACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC <th>540</th>	540
Qy	Db	481	GTGACAGACAGAACCCCAAGAACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC <th>540</th>	540
Qy	Db	541	CAAAATCTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTAC <th>600</th>	600
Qy	Db	541	CAAAATCTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTAC <th>600</th>	600

601 CTGCTAGCACTGGTACAGAGCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
601 CTGCTAGCACTGGTACAGAGCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
661 GGTTCGCTTTGTGAGTACAGAGCAATCTTGGAAATTCAGGCGATACCCGGGAGCAGTC 720
661 GGTTCGCTTTGTGAGTACAGAGCAATCTTGGAAATTCAGGCGATACCCGGGAGCAGTC 720
721 AGGGACTACGAGTGCAGTGCCTCCATGACGTGCGCGCGCGCTGTGTACGGAGATAA 780
721 AGGGACTACGAGTGCAGTGCCTCCATGACGTGCGCGCGCGCTGTGTACGGAGATAA 780
781 GGTCAACGTCAGTATCCACCATATCTTTCAGAGCAAGGAGTACAGTGTCCCGTGG 840
781 GGTCAACGTCAGTATCCACCATATCTTTCAGAGCAAGGAGTACAGTGTCCCGTGG 840
841 ACAAAAGGGGACACTGCAGTGTGAAGCTTCAGAGTCCCTCCAGCAGAAATTCAGTGTGA 900
841 ACAAAAGGGGACACTGCAGTGTGAAGCTTCAGAGTCCCTCCAGCAGAAATTCAGTGTGA 900
901 CAAGGATGACAAAGAGCTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTT 960
901 CAAGGATGACAAAGAGCTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTT 960
961 CTTCTCAAACTCATCTCTCAATGCTCTGACATGATGCGAGTATTTGGTCCAGCGCGCT 1020
961 CTTCTCAAACTCATCTCTCAATGCTCTGACATGATGCGAGTATTTGGTCCAGCGCGCT 1020
1021 GCGCTCCCAAGGAGTGGGACACCAATGCCAGATGATGCTATTTGGTCCAGCGCGCT 1080
1021 GCGCTCCCAAGGAGTGGGACACCAATGCCAGATGATGCTATTTGGTCCAGCGCGCT 1080
1081 CAGCAGGTGAGCAAGGAGTGGGACACCAATGCCAGATGATGCTATTTGGTCCAGCGCT 1140
1081 CAGCAGGTGAGCAAGGAGTGGGACACCAATGCCAGATGATGCTATTTGGTCCAGCGCT 1140
1141 GGTCTGCACTGCTTCTCAATTTTGTGATGATGCTGCTCCATCCCGGAGGAGCT 1200
1141 GGTCTGCACTGCTTCTCAATTTTGTGATGATGCTGCTCCATCCCGGAGGAGCT 1200
1201 GCGGCAACCAAGGAGTGGGACACCAATGCCAGATGATGCTATTTGGTCCAGCGCT 1260
1201 GCGGCAACCAAGGAGTGGGACACCAATGCCAGATGATGCTATTTGGTCCAGCGCT 1260
1261 TATACAAATGAAATGAGAAACACAGAGTGGGACACCAATGCCAGATGATGCTATTTGGTCCAGCGCT 1320
1261 TATACAAATGAAATGAGAAACACAGAGTGGGACACCAATGCCAGATGATGCTATTTGGTCCAGCGCT 1320
1321 AAAGATCTTTGGGGGAAAGAGTGTAAAGAGAAATTTGAAATTCCTTGCAGATA 1380
1321 AAAGATCTTTGGGGGAAAGAGTGTAAAGAGAAATTTGAAATTCCTTGCAGATA 1380
1381 TTTAGTACATGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1440
1381 TTTAGTACATGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1440
1441 CCACTGCAAGTGTGAGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1500
1441 CCACTGCAAGTGTGAGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1500
1501 TCTGCCACAGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1560
1501 TCTGCCACAGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1560
1561 GTCCATGAGAGACAGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1620
1561 GTCCATGAGAGACAGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1620
1621 GTAGCTGTGCCACAGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1679
1621 GTAGCTGTGCCACAGAGTGTCTTTTCCCAAGGAGGAGACACAGCAGCAGCAGCGCTTGA 1679

RESULT 5
US-09-978-189-522
Sequence 522, Application US/09978189
Publication No. US20030040102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deshoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei Qiang
APPLICANT: Gerstein, Hanseter
APPLICANT: Gottesman, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27

Best Local Similarity 100.0%; Pred. No. 1.7e-150; Mismatches 0; Indels 0; Gaps 0; Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTQPKHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
 DB 1 MKTQPKHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
 QY 61 NRVTRVWLNRSITLYAGNDKWCIDPRVLLSNTQYSEIQNDVYDEGPTCSVQTD 120
 DB 61 NRVTRVWLNRSITLYAGNDKWCIDPRVLLSNTQYSEIQNDVYDEGPTCSVQTD 120
 QY 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHHISPKAVGFV 180
 DB 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHHISPKAVGFV 180
 QY 181 SEDEYLEIOGITREOSGDYECSSANDVAAPVVRVVKVTVNYPPISEAKGTGVPVQKGT 240
 DB 181 SEDEYLEIOGITREOSGDYECSSANDVAAPVVRVVKVTVNYPPISEAKGTGVPVQKGT 240
 QY 241 LQCEASAVPSAEFOWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 DB 241 LQCEASAVPSAEFOWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 QY 301 LGHTNASIMLFGPGAVSEVSNGTSSRRAGCVWLLPLLVLLHLLKF 344
 DB 301 LGHTNASIMLFGPGAVSEVSNGTSSRRAGCVWLLPLLVLLHLLKF 344

RESULT 7

US-09-978-585A-523
 : Sequence 523, Application US/0978585A
 : Publication No. US20030049633A1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi
 : APPLICANT: Baker Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan
 : APPLICANT: Ferrara, Napoleon
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Gerritsen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Kijavin, Ivar J.
 : APPLICANT: Kuo, Sophia S.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Shelton, David L.
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 : FILE REFERENCE: P2630PIC15
 : CURRENT APPLICATION NUMBER: US/09/978, 585A
 : CURRENT FILING DATE: 2001-10-16
 : NUMBER OF SEQ ID NOS: 624
 : Prior Application removed - See File Wrapper or Palm
 : SEQ ID NO 523
 : LENGTH: 344
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-978-585A-523

Query Match 100.0%; Score 1806; DB 11; Length 344; Best Local Similarity 100.0%; Pred. No. 1.7e-150; Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTQPKHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
 DB 1 MKTQPKHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
 QY 61 NRVTRVWLNRSITLYAGNDKWCIDPRVLLSNTQYSEIQNDVYDEGPTCSVQTD 120
 DB 61 NRVTRVWLNRSITLYAGNDKWCIDPRVLLSNTQYSEIQNDVYDEGPTCSVQTD 120
 QY 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHHISPKAVGFV 180
 DB 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHHISPKAVGFV 180
 QY 181 SEDEYLEIOGITREOSGDYECSSANDVAAPVVRVVKVTVNYPPISEAKGTGVPVQKGT 240
 DB 181 SEDEYLEIOGITREOSGDYECSSANDVAAPVVRVVKVTVNYPPISEAKGTGVPVQKGT 240
 QY 241 LQCEASAVPSAEFOWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 DB 241 LQCEASAVPSAEFOWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 QY 301 LGHTNASIMLFGPGAVSEVSNGTSSRRAGCVWLLPLLVLLHLLKF 344
 DB 301 LGHTNASIMLFGPGAVSEVSNGTSSRRAGCVWLLPLLVLLHLLKF 344

RESULT 8

US-09-978-191A-523
 : Sequence 523, Application US/0978191A
 : Publication No. US20030050239A1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi
 : APPLICANT: Baker Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan
 : APPLICANT: Ferrara, Napoleon
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Gerritsen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Kijavin, Ivar J.
 : APPLICANT: Kuo, Sophia S.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Shelton, David L.
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 : FILE REFERENCE: P2630PIC4
 : CURRENT APPLICATION NUMBER: US/09/978,191A
 : CURRENT FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 09/918585
 : PRIOR FILING DATE: 2001-07-30
 : PRIOR APPLICATION NUMBER: 60/062250
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/064249
 : PRIOR FILING DATE: 1997-11-03
 : PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
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 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
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 PRIOR FILING DATE: 1998-05-06
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 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
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 PRIOR APPLICATION NUMBER: 60/084643
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 PRIOR APPLICATION NUMBER: 60/085338
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 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.7e-150;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKTQPKMHSISWAIFTGLAALCLFQGVPRSGDATFFPKAMDNVTVRQGESATLRCTID 60
 Db 1 MKTQPKMHSISWAIFTGLAALCLFQGVPRSGDATFFPKAMDNVTVRQGESATLRCTID 60
 Qy 61 NVTTRVWLNRSTILYAGNDKWCIDPRVLLSNTQYSEIQNVVDVYDEGPTCSVQTD 120
 Db 61 NVTTRVWLNRSTILYAGNDKWCIDPRVLLSNTQYSEIQNVVDVYDEGPTCSVQTD 120
 Qy 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 Db 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 Qy 181 SEDEYLEIQITREQSDYECASNDVAAPVVRVKVTVVYPPYISEAKGTGVPVGOKGT 240
 Db 181 SEDEYLEIQITREQSDYECASNDVAAPVVRVKVTVVYPPYISEAKGTGVPVGOKGT 240
 Qy 241 LOCASAVPSAEFQWYKDDKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 Db 241 LOCASAVPSAEFQWYKDDKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 Qy 301 LGHTNASIMLFGPGAVSEVSNSTSRACGCVWLLPLLVHLLKLF 344
 Db 301 LGHTNASIMLFGPGAVSEVSNSTSRACGCVWLLPLLVHLLKLF 344

RESULT 6

US-09-978-608A-523
 ; Sequence 523, Application US/09978608A
 ; Publication No. US20030045462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630F1C22
 ; CURRENT APPLICATION NUMBER: US/09/978,608A
 ; CURRENT FILING DATE: 2001-10-16
 ; NUMBER OF SEQ ID NOS: 624
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 523
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-978-608A-523

Query Match

100.0%; Score 1806; DB 11; Length 344;

OY 181 SEDEVLEIQTREOSGDYECASNDVAAPVVRKVTVNYPPISEAKGTGVPVGOKGT 240
 Db 181 SEDEVLEIQTREOSGDYECASNDVAAPVVRKVTVNYPPISEAKGTGVPVGOKGT 240
 OY 241 LOCASAVPSAEQWYKDDKRLIECKGKVKNRPFLSKLIFFNVSEHDYNTCVASNK 300
 Db 241 LOCASAVPSAEQWYKDDKRLIECKGKVKNRPFLSKLIFFNVSEHDYNTCVASNK 300
 OY 301 LGHNASIMLFGGAVSEVSGTSSRACGVWLLPLVLVHLHLKF 344
 Db 301 LGHNASIMLFGGAVSEVSGTSSRACGVWLLPLVLVHLHLKF 344

RESULT 5

US-09-189-189-523
 ; Sequence 523, Application US/09978189
 ; Publication No. US20030004102A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gertschen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Hune, Auscin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavir, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C7
 CURRENT APPLICATION NUMBER: US/09/978,189
 PRIOR FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 10; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.7e-150;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 M K T I O P K M H N S I S W A I F T G L A A C L F Q C V P V R S D A T F P K A N D N V T V R Q G S A T L R C T I D 60
 Db 1 M K T I O P K M H N S I S W A I F T G L A A C L F Q C V P V R S D A T F P K A N D N V T V R Q G S A T L R C T I D 60
 Qy 61 N E V T R V A W L A R S T I L Y A G N D K W C L D P R V L L S N T O Y S I E I O N V D Y D E G P Y T C S V Q T D 120
 Db 61 N E V T R V A W L A R S T I L Y A G N D K W C L D P R V L L S N T O Y S I E I O N V D Y D E G P Y T C S V Q T D 120
 Qy 121 N H P K T S R V H L I V Q S P K I V E I S S D I S I N E G N N I S L T C I A T G R P E P T V T W R H I S P K A V G E V 180
 Db 121 N H P K T S R V H L I V Q S P K I V E I S S D I S I N E G N N I S L T C I A T G R P E P T V T W R H I S P K A V G E V 180

PRIOR FILING DATE: 1998-04-29
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 10; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.7e-150;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKTIOPKMHSISWAIFTGLAALCLFQGVPRVRS	60
DB	1	MKTIOPKMHSISWAIFTGLAALCLFQGVPRVRS	60
QY	61	NRVTRVAMLRSTILYAGNDKWCIDPRVLLSNTOTQY	120
DB	61	NRVTRVAMLRSTILYAGNDKWCIDPRVLLSNTOTQY	120
QY	121	NHPTKSRVHLIVQSPKIVISDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV	180
DB	121	NHPTKSRVHLIVQSPKIVISDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV	180
QY	181	SEDEYLETOGTRQSGDYECSSASNDVAAAPVVRVKKVTYVNPYPISEAKGTGVPVQKGT	240
DB	181	SEDEYLETOGTRQSGDYECSSASNDVAAAPVVRVKKVTYVNPYPISEAKGTGVPVQKGT	240
QY	241	LOCEASAVPSAEFFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNK	300
DB	241	LOCEASAVPSAEFFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNK	300
QY	301	LGTNASIMLFGPAGVSEVSNGTSSRAGCVWLLPLVLHLLKF	344
DB	301	LGTNASIMLFGPAGVSEVSNGTSSRAGCVWLLPLVLHLLKF	344

RESULT 4
 US-09-999-932A-523
 ; Sequence 523, Application US/09999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, AVI
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurley, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC63
 ; CURRENT APPLICATION NUMBER: US/09/999,832A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Roy, Margaret Ann
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APPLICANT: Stewart, Timothy A.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P199
CURRENT FILING DATE: 2001-10-15
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 1806; DB 10; Length 344;
 Best Local Similarity 100.0% Pred. No. 1, 7e-150;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	NRTVAVLNRSTILVAGNDKWCPLDPRVLLSNTQTOYSIEIONVDYDEGPTCSVQTD	120
Db	61	NRTVAVLNRSTILVAGNDKWCPLDPRVLLSNTQTOYSIEIONVDYDEGPTCSVQTD	120
Qy	121	NHPTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV	180
Db	121	NHPTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV	180
Qy	181	SEDEYLEIQITREQSGDYECSSANDVAAPVVRVKVTVNYPPIYSEAKGTGVPVGQGT	240
Db	181	SEDEYLEIQITREQSGDYECSSANDVAAPVVRVKVTVNYPPIYSEAKGTGVPVGQGT	240
Qy	241	LQCEASAVPSAEQWYKDDKRLIEGKGVKVENRPFSLKLIFFNYSYHDYGNVTCVASNK	300
Db	241	LQCEASAVPSAEQWYKDDKRLIEGKGVKVENRPFSLKLIFFNYSYHDYGNVTCVASNK	300
Qy	301	LCHTNASIMLFGPGAVSEVSNCTSRACGVYLLPLLVLLHLLKF	344
Db	301	LCHTNASIMLFGPGAVSEVSNCTSRACGVYLLPLLVLLHLLKF	344

RESULT 3
 US-09-978-192A-523
 ; Sequence 523, Application US/05978192A
 ; Patent No. US20020177553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen


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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1806; DB 10; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 M K T I O P K M H N S I W A I F T G L A A L C L F Q G V P V R S G D A T F P K A M D N V T V R G E S A T L R C T I D 60
QY 61 N R V T R V A M L N S T I L Y A G N D K W C L D P R V V L L S N T O T O Y S I E I O N V D V D E G F Y T C S V Q T D 120
DB 61 N R V T R V A M L N S T I L Y A G N D K W C L D P R V V L L S N T O T O Y S I E I O N V D V D E G F Y T C S V Q T D 120
QY 121 N H P K T S R V H L I V Q S P K I V E I S D I S I N E G N N I S L T C I A T G R P E P T V T W R H I S P K A V G F V 180
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DB 181 S E D V L E I Q G T I R E O S G D Y E C S A N D V A P V R V R K V T V N Y P P Y I S E A K G T G V P V G Q K G T 240
QY 241 L O C E A S A N P S A F E F O W Y K D K R L I E G K G V K V E N P F S K L I F F N V S E H D Y G N Y T C V A S N K 300
DB 241 L O C E A S A N P S A F E F O W Y K D K R L I E G K G V K V E N P F S K L I F F N V S E H D Y G N Y T C V A S N K 300
QY 301 L G H T N A S I M L F G C A V S E V S N G T S R A C C V W L L L L V L L H L L K F 344
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RESULT 2
US-09-978-697-523
Sequence 523, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottschalk, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;

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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333

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GenCore version 5.1.6
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Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	1806	100.0	344	10	US-09-978-192A-523
4	1806	100.0	344	10	US-09-999-832A-523
5	1806	100.0	344	11	US-09-978-189-523
6	1806	100.0	344	11	US-09-978-608A-523
7	1806	100.0	344	11	US-09-978-585A-523
8	1806	100.0	344	11	US-09-978-131A-523
9	1806	100.0	344	11	US-09-978-564A-523
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45	1806	100.0	344	12	US-10-145-746-376

ALIGNMENTS

RESULT 1

US-09-978-295A-523
Sequence 523 Application US/09978295A
Accession US20030156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2630P11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-414-657D-56

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Best Local Similarity 56.9%; Pred. No. 1.3e-71;
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DB 61 EGSYTCVSQTDNHPKTSRHLIVQVSPKIVEISDISINEGNISLTCTATGRPEPTVTW 120
QY 170 RHISPRKGVFSEDEYLEIQITREQSGDYECASNDVAAPVRRVKVTVNYPPISEAK 229
DB 121 RHLTPGTREGESEYLEILGITREQSGDYECASNDVAAPVRRVKVTVNYPPISEAK 180
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DB 181 SNEATTGQASLKCEASAVPDPFWEYRDDTR-INSANGLEIKSTEGQSSLTVTNVTTEH 239
QY 290 YGNYTCVASNKLK 302
DB 240 YGNYTCVASNKLK 252

Search completed: September 11, 2003, 03:06:30
Job time : 36 secs

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 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
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 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 287 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-414-657D-48

Query Match 49.18; Score 886.5; DB 2; Length 287;
 Best Local Similarity 56.6%; Pred. No. 1.6e-80;
 Matches 164; Conservative 57; Mismatches 66; Indels 3; Gaps 2;
 QY 31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSITLYAGNDKWCIDPRVYL 90
 DB 1 VRSD--FNRGTDNITVRQGDATLRVLEDKNSKAVLNRSIGIIFAGHDKWSLDPRVEL 58
 QY 91 LSNTOQYSTEIQNDVYDEGPYTCVSQTDNHPKTSRVHLIVQVSPKIYEISSDISINEG 150
 DB 59 EKRLSLEYSLRIQKVDVDEGYSYCSVQTHPEKTSQVYLIVQVPPKISNISSDVTYNEG 118
 QY 151 NNISLTCTATGRPEPTVTRHRSIPKAVGFVSEDEYLEIOGITREQSGDYECASNDVAAP 210
 DB 119 SNVTLVCMANGRPVITVRHLTPGREFEGEEYLEILGITREQSGKYCKEAAVESSA 178
 QY 211 VVRVKVTVNVPYIPISAKGTGVPVGOKGTQCEASAVPSAEFQYKDDKRLIEGKGVK 270
 DB 179 DYKQKVTVNVPPTITESKNEATTGQASLKCEASAVPAPDFEYTRDTR-INSANGLE 237
 QY 271 VNRPLSKLIFFNVSEHDYGNVTCVASKLGHNTNASIMLFGGAVSEVS 320
 DB 238 IKSTEGQSSLTVTNVTTEHYGNTVCAANKLGVTNASLVLFRPGSVRGIN 287

RESULT 14
 US-08-414-657D-49
 ; Sequence 49, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA

; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,657D
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 49:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 287 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-414-657D-49

Query Match 49.08; Score 885.5; DB 2; Length 287;
 Best Local Similarity 56.6%; Pred. No. 2e-80;
 Matches 164; Conservative 57; Mismatches 66; Indels 3; Gaps 2;
 QY 31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSITLYAGNDKWCIDPRVYL 90
 DB 1 VRSD--FNRGTDNITVRQGDATLRVLEDKNSKAVLNRSIGIIFAGHDKWSLDPRVEL 58
 QY 91 LSNTOQYSTEIQNDVYDEGPYTCVSQTDNHPKTSRVHLIVQVSPKIYEISSDISINEG 150
 DB 59 EKRLSLEYSLRIQKVDVDEGYSYCSVQTHPEKTSQVYLIVQVPPKISNISSDVTYNEG 118
 QY 151 NNISLTCTATGRPEPTVTRHRSIPKAVGFVSEDEYLEIOGITREQSGDYECASNDVAAP 210
 DB 119 SNVTLVCMANGRPVITVRHLTPGREFEGEEYLEILGITREQSGKYCKEAAVESSA 178
 QY 211 VVRVKVTVNVPYIPISAKGTGVPVGOKGTQCEASAVPSAEFQYKDDKRLIEGKGVK 270
 DB 179 DYKQKVTVNVPPTITESKNEATTGQASLKCEASAVPAPDFEYTRDTR-INSANGLE 237
 QY 271 VNRPLSKLIFFNVSEHDYGNVTCVASKLGHNTNASIMLFGGAVSEVS 320
 DB 238 IKSTEGQSSLTVTNVTTEHYGNTVCAANKLGVTNASLVLFRPGSVRGIN 287

RESULT 15
 US-08-414-657D-56
 ; Sequence 56, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60

STATE: NJ
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 310 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-414-657D-45

Query Match 50.1%; Score 905; DB 2; Length 310;
 Best Local Similarity 55.3%; Pred. No. 2.5e-82;
 Matches 173; Conservative 59; Mismatches 77; Indels 4; Gaps 3;
 QY 31 VRSGDATPKAMDNVVRQGESATLRCTIDNRVTRVAMLNKSTLYAGNDKWLDPVVL 90
 DB 1 VRSD--FNRGDTNIVRQGDATLRCLVLEDKNSKVAWLNKSGIIFAGHDKWSDPVEL 58
 QY 91 LSWTQYISIQNVVDYDEGPTCSVOTDNHPKTSRVHLIVQVSPKIVESSDISINEG 150
 DB 59 EKRAHLYSLRIQKVVDYDEGSTCSVOTQHEPKTSQVYLIVQVPPKINSISDVTVNEG 118
 QY 151 NNSITCIATGRPEPTVTRHISPKAVGVSEDEYLEIQITREOSGDYECASNDVAAP 210
 DB 119 SNVTLVCMANGRPEPTVTRHILTPGREFEGEEYLEILGITREOSGYECKAAEVSSA 178
 QY 211 VVRVKVTNVPYPISEAKGTGVPVQKGTLOCEASAVPSAEFQYKDDKRLIEGKGVK 270
 DB 179 DVQVKVTNVPPTITESKSNEATTGROASLKCEASAVPAPDFEYRDDTR-INSANGLE 237
 QY 271 VNRPFSLKLIFFNVSHDYGNYTCVASKNKLGHNTASIMLFGAVSEVSGTSSRAGCV 330
 DB 238 IKSTEGQSSLLVTNVTBEEHYGNYTCVAANKLGVTNASLVLFPRGVSVRGI-NGSISLA 296
 QY 331 WLLPLVLLHLK 343
 DB 297 WLLAASLFLCLK 309

RESULT 12
 US-08-414-657D-44
 Sequence 44, Application US/08414657D
 Patent No. 5861283
 GENERAL INFORMATION:
 APPLICANT: Levitt, Pat
 APPLICANT: Pimenta, Aurea
 APPLICANT: Zhukareva, Izhak
 TITLE OF INVENTION: Limbic System-Associated Membrane
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:

ADDRESS: Dechert, Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 304 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-414-657D-44

Query Match 49.9%; Score 902; DB 2; Length 304;
 Best Local Similarity 55.5%; Pred. No. 4.8e-82;
 Matches 171; Conservative 59; Mismatches 74; Indels 4; Gaps 3;
 QY 31 VRSGDATPKAMDNVVRQGESATLRCTIDNRVTRVAMLNKSTLYAGNDKWLDPVVL 90
 DB 1 VRSD--FNRGDTNIVRQGDATLRCLVLEDKNSKVAWLNKSGIIFAGHDKWSDPVEL 58
 QY 91 LSWTQYISIQNVVDYDEGPTCSVOTDNHPKTSRVHLIVQVSPKIVESSDISINEG 150
 DB 59 EKRAHLYSLRIQKVVDYDEGSTCSVOTQHEPKTSQVYLIVQVPPKINSISDVTVNEG 118
 QY 151 NNSITCIATGRPEPTVTRHISPKAVGVSEDEYLEIQITREOSGDYECASNDVAAP 210
 DB 119 SNVTLVCMANGRPEPTVTRHILTPGREFEGEEYLEILGITREOSGYECKAAEVSSA 178
 QY 211 VVRVKVTNVPYPISEAKGTGVPVQKGTLOCEASAVPSAEFQYKDDKRLIEGKGVK 270
 DB 179 DVQVKVTNVPPTITESKSNEATTGROASLKCEASAVPAPDFEYRDDTR-INSANGLE 237
 QY 271 VNRPFSLKLIFFNVSHDYGNYTCVASKNKLGHNTASIMLFGAVSEVSGTSSRAGCV 330
 DB 238 IKSTEGQSSLLVTNVTBEEHYGNYTCVAANKLGVTNASLVLFPRGVSVRGI-NGSISLA 296
 QY 331 WLLPLVLL 338
 DB 297 WLLAASLL 304

RESULT 13
 US-08-414-657D-48
 Sequence 48, Application US/08414657D
 Patent No. 5861283
 GENERAL INFORMATION:
 APPLICANT: Levitt, Pat
 APPLICANT: Pimenta, Aurea
 APPLICANT: Fischer, Itzhak
 APPLICANT: Zhukareva, Victoria
 TITLE OF INVENTION: Limbic System-Associated Membrane

OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414/657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:

INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 308 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-414-657D-46

Query Match 50.3%; Score 908; DB 2; Length 308;
 Best Local Similarity 56.3%; Pred. No. 1.2e-82;
 Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;
 QY 20 LAALCLF-QGVPRSGDATFFKAMDNTVROGESATLRCTDNRVTRVAVLNRSSTLYAG 78
 DB 10 LRLCLLPTGLPVRSVD--FNRGTDNITVRGDTAILRCVLEDKSKVAVLNRSSTLYAG 67
 QY 79 NDKWCLDPRVLLSNTQYSEIQNDVYDEGPTVCSVQTDNHPKTSRVHLIVQVSPKI 138
 DB 68 HAWSLDPRVLEKRSLSLEYSLRQKVDYDEGPTVCSVQTOHEPKTSQVYLIIVQVPPKI 127
 QY 139 VEISSDISINEGNISLCTATGRPEPTVTRHHSIPKAVGFVSEDEYLEIGITREQSGD 198
 DB 128 SNISDDVTNVEGNSVTLVCMANGREPVTITWRHLTPGREFEGEEYLEIGITREQSGK 187
 QY 199 YECASNDVAAPVRRVRYVYPPYISEAKGTGVPVGOKGTLOCEASVPSAEFOYKND 258
 DB 188 YECCAANEVSSADVQVKVTVNYPPTITESKNEATTGROASLKCEASVAPDFEYWRD 247
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNGLGHTNASIMLFGPGAYSE 318
 DB 248 DTR-INSANGLEIKSTEGSSLTNTVNTTEHYGNTCTVAANKLGVTNASILVLRPGSVRG 306
 QY 319 VS 320
 DB 307 IN 308

RESULT 10
 US-08-414-657D-47
 Sequence 47, Application US/08414657D
 Patent No. 5861283
 GENERAL INFORMATION:
 APPLICANT: Levitt, Pat
 APPLICANT: Pimenta, Aurea
 APPLICANT: Fischer, Itzhak
 APPLICANT: Zhukareva, Victoria
 TITLE OF INVENTION: Limbic System-Associated Membrane
 TITLE OF INVENTION: Protein and DNA
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 STATE: NJ
 COUNTRY: USA
 ZIP: 08543

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414/657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 315 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-414-657D-47

Query Match 50.2%; Score 907; DB 2; Length 315;
 Best Local Similarity 56.3%; Pred. No. 1.6e-82;
 Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;
 QY 20 LAALCLF-QGVPRSGDATFFKAMDNTVROGESATLRCTDNRVTRVAVLNRSSTLYAG 78
 DB 17 LRLCLLPTGLPVRSVD--FNRGTDNITVRGDTAILRCVLEDKSKVAVLNRSSTLYAG 74
 QY 79 NDKWCLDPRVLLSNTQYSEIQNDVYDEGPTVCSVQTDNHPKTSRVHLIVQVSPKI 138
 DB 75 HKWSLDPRVLEKRSLSLEYSLRQKVDYDEGPTVCSVQTOHEPKTSQVYLIIVQVPPKI 134
 QY 139 VEISSDISINEGNISLCTATGRPEPTVTRHHSIPKAVGFVSEDEYLEIGITREQSGD 198
 DB 135 SNISDDVTNVEGNSVTLVCMANGREPVTITWRHLTPGREFEGEEYLEIGITREQSGK 194
 QY 199 YECASNDVAAPVRRVRYVYPPYISEAKGTGVPVGOKGTLOCEASVPSAEFOYKND 258
 DB 195 YECCAANEVSSADVQVKVTVNYPPTITESKNEATTGROASLKCEASVAPDFEYWRD 254
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNGLGHTNASIMLFGPGAYSE 318
 DB 255 DTR-INSANGLEIKSTEGSSLTNTVNTTEHYGNTCTVAANKLGVTNASILVLRPGSVRG 313
 QY 319 VS 320
 DB 314 IN 315

RESULT 11
 US-08-414-657D-45
 Sequence 45, Application US/08414657D
 Patent No. 5861283
 GENERAL INFORMATION:
 APPLICANT: Levitt, Pat
 APPLICANT: Pimenta, Aurea
 APPLICANT: Fischer, Itzhak
 APPLICANT: Zhukareva, Victoria
 TITLE OF INVENTION: Limbic System-Associated Membrane
 TITLE OF INVENTION: Protein and DNA
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/135,080
;; FILING DATE: 17-AUG-1998
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA: 08/414,657
;; FILING DATE: 31-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bloom, Allen
;; REGISTRATION NUMBER: 29,135
;; REFERENCE/DOCKET NUMBER: 317743-102
;; TELEPHONE: 609-520-3214
;; TELEFAX: 609-520-3259
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 60:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 338 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-414-657D-60

Query Match 51.1%; Score 923.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred No. 4e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;
QY 20 LAALCLF-QGVPRSGDATFPKANDNTVROGESATLRCIDNRVTRVAMLNRSITLYAG 78
DB 17 LRLCLPTGLPRVSD--FNRGDNITVRQDYLKCVLEDKNSKVAWLNRSIGIFAG 74
QY 79 NDKWCLDPVLLSNTQYISIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKWSLDPRVLEKRSLSYLRQKVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 134
QY 139 VEISDISINEGNISLTCATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
DB 135 SNISDVTVNEGSNTVLCMANGRPPEVITWRHLTPGREFEGEEYLEILGITREQSGK 194
QY 199 YECASNDVAAPVRRVKVTNYPPIYSEAKGTGVPVQKGTQCEASAVPSAEFQYKD 258
DB 195 YECKAANEVSSADVKQVKVTNYPPTITESKSNEATTGROASLKCEASAVPAPDFEYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASIMLFGPGAYSE 318
DB 255 DTR-INSANGLEIKSTEGOSLTVMTVEEHYGNVTCVAAKLGVTNASLVLFPRGVRG 313
QY 319 VSGTERRAGCVWLLPLLVHLHLK 343
DB 314 I-NGSISLAVPLWLLAASLLCLSK 337

RESULT 8
US-09-135-080-8
; Sequence 8, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/135,080
;; FILING DATE: 17-AUG-1998
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA: 08/414,657
;; FILING DATE: 31-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bloom, Allen
;; REGISTRATION NUMBER: 29,135
;; REFERENCE/DOCKET NUMBER: 317743-102A
;; TELEPHONE: 609-620-3214
;; TELEFAX: 609-620-3259
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 338 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-09-135-080-8

Query Match 51.1%; Score 923.5; DB 4; Length 338;
Best Local Similarity 55.1%; Pred No. 4e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;
QY 20 LAALCLF-QGVPRSGDATFPKANDNTVROGESATLRCIDNRVTRVAMLNRSITLYAG 78
DB 17 LRLCLPTGLPRVSD--FNRGDNITVRQDYLKCVLEDKNSKVAWLNRSIGIFAG 74
QY 79 NDKWCLDPVLLSNTQYISIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKWSLDPRVLEKRSLSYLRQKVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 134
QY 139 VEISDISINEGNISLTCATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
DB 135 SNISDVTVNEGSNTVLCMANGRPPEVITWRHLTPGREFEGEEYLEILGITREQSGK 194
QY 199 YECASNDVAAPVRRVKVTNYPPIYSEAKGTGVPVQKGTQCEASAVPSAEFQYKD 258
DB 195 YECKAANEVSSADVKQVKVTNYPPTITESKSNEATTGROASLKCEASAVPAPDFEYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASIMLFGPGAYSE 318
DB 255 DTR-INSANGLEIKSTEGOSLTVMTVEEHYGNVTCVAAKLGVTNASLVLFPRGVRG 313
QY 319 VSGTERRAGCVWLLPLLVHLHLK 343
DB 314 I-NGSISLAVPLWLLAASLLCLSK 337

RESULT 9
US-08-414-657D-46
; Sequence 46, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-414-657D-41

Query Match 51.1%; Score 923.5; DB 2; Length 325;
Best Local Similarity 55.3%; Pred. No. 3.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATTFFPKAMNDVTVRQGESATLCTIDNRVTRVAMLRSTILYAG 78
DB 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQDGTALRCVLEDKNSKVAMLRSGIIFAG 67
QY 79 NDKWCLDPVLLSNTQTOYSIEIQNVVDYDEGPTCSVOTDNHPTKSRVHLIVQVSPKI 138
DB 68 HDKWSLDPRVLEKRLHSLEYSLRIOKVVDYDEGPTCSVOTQHEPKTSQVYLIVQVPEKI 127
QY 139 VEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEIOGITREQSGD 198
DB 128 SNSSDVTNVEGNSVTLVCMANGRPVITWRHLPTTGREFEGEEYLEILGITREQSGK 187
QY 199 YECASNDVAAPVVRKVTNYPPIYSEAKGTGVPVGOKTQCEASAVPSAEFQWKD 258
DB 188 YECCAANEVSSADVKQKVTNYPPTITESKNEATTTGROASLKCEASAVPADPEWYRD 247
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKGHTNASIMLFGPQVSE 318
DB 248 DTR-INSANGLEIKSTEGQSSLTNTVTEEHYGNVTCVANKLGVTNASLVLFRPGSVRG 306
QY 319 VSGTSTRRACGVLLPLVL 338
DB 307 I-NGSISLAVPLMLLAASLL 325

RESULT 6

US-09-135-080-2
Sequence 2, Application US/09135080
Patent No. 6423827
GENERAL INFORMATION:
APPLICANT: Levitt, Pat R.
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 17-AUG-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
TELEFAX: 609-620-3259
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-135-080-2

Query Match 51.1%; Score 923.5; DB 4; Length 325;
Best Local Similarity 55.3%; Pred. No. 3.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATTFFPKAMNDVTVRQGESATLCTIDNRVTRVAMLRSTILYAG 78
DB 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQDGTALRCVLEDKNSKVAMLRSGIIFAG 67
QY 79 NDKWCLDPVLLSNTQTOYSIEIQNVVDYDEGPTCSVOTDNHPTKSRVHLIVQVSPKI 138
DB 68 HDKWSLDPRVLEKRLHSLEYSLRIOKVVDYDEGPTCSVOTQHEPKTSQVYLIVQVPEKI 127
QY 139 VEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEIOGITREQSGD 198
DB 128 SNSSDVTNVEGNSVTLVCMANGRPVITWRHLPTTGREFEGEEYLEILGITREQSGK 187
QY 199 YECASNDVAAPVVRKVTNYPPIYSEAKGTGVPVGOKTQCEASAVPSAEFQWKD 258
DB 188 YECCAANEVSSADVKQKVTNYPPTITESKNEATTTGROASLKCEASAVPADPEWYRD 247
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKGHTNASIMLFGPQVSE 318
DB 248 DTR-INSANGLEIKSTEGQSSLTNTVTEEHYGNVTCVANKLGVTNASLVLFRPGSVRG 306
QY 319 VSGTSTRRACGVLLPLVL 338
DB 307 I-NGSISLAVPLMLLAASLL 325

RESULT 7

US-08-414-657D-60
Sequence 60, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435

US-09-135-080-4
 TOPOLOGY: linear
 Query Match 51.3%; Score 926.5; DB 4; Length 338;
 Best Local Similarity 55.1%; Pred. No. 2e-84;
 Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;
 QY 20 LAALCLF-OGVPRSGDATFPKANDNTVROGESATRLCTIDNRVTRVAWLNSTLYAG 78
 DB 17 LRLCLLFTGLPVSVD--FNRTDNITVRQDTRAILRVCVDEKSKVAWLNRSGLIFAG 74
 QY 79 NDKWGLDPRVLLSNTQTSYIEIQNDYVDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
 DB 75 HKNWGLDPRVLEKRAHLEYSRLQKVDYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 134
 QY 139 VEISSDINSNGNISLCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIOGTREOSGD 198
 DB 135 SNISSDVTNNGSVNLTVCANGRPVITWRHLTPGREFEGEEYLEILGITREOSGK 194
 QY 199 YECASNDVAAPVRRVVKVTNVPYIIEAKGTGVPVQKGTLCQCEASAVPSAEFQWYKD 258
 DB 195 YECKAANEVSSADVKQVKTVPYPTITESKSNBATTGRQASLKCEASAVPAPDFEYRD 254
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKGHTNASIMLFGPGVASE 318
 DB 255 DTR-INSANGLEIKSTEGQSSLTVTNVTTEHYGNVTCVAAANKLGVTNASLVLPFGSVRG 313
 QY 319 VSNGTSRAGCVWLLPLVLLK 343
 DB 314 I-NGSISLAVPLWLLAASLFLCLK 337

RESULT 4
 US-08-414-657D-2
 Sequence 2, Application US/08414657D
 Patent No. 5861283
 GENERAL INFORMATION:
 APPLICANT: Levitt, Pat
 APPLICANT: Pimenta, Aurea
 APPLICANT: Fischer, Itzhak
 APPLICANT: Zhukareva, Victoria
 TITLE OF INVENTION: Limbic System-Associated Membrane
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION NUMBER:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-414-657D-2
 Query Match 51.1%; Score 923.5; DB 2; Length 325;
 Best Local Similarity 55.3%; Pred. No. 3.8e-84;
 Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;
 QY 20 LAALCLF-OGVPRSGDATFPKANDNTVROGESATRLCTIDNRVTRVAWLNSTLYAG 78
 DB 10 LRLCLLFTGLPVSVD--FNRTDNITVRQDTRAILRVCVDEKSKVAWLNRSGLIFAG 67
 QY 79 NDKWGLDPRVLLSNTQTSYIEIQNDYVDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
 DB 68 HKNWGLDPRVLEKRAHLEYSRLQKVDYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127
 QY 139 VEISSDINSNGNISLCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIOGTREOSGD 198
 DB 138 SNISSDVTNNGSVNLTVCANGRPVITWRHLTPGREFEGEEYLEILGITREOSGK 187
 QY 199 YECASNDVAAPVRRVVKVTNVPYIIEAKGTGVPVQKGTLCQCEASAVPSAEFQWYKD 258
 DB 188 YECKAANEVSSADVKQVKTVPYPTITESKSNBATTGRQASLKCEASAVPAPDFEYRD 247
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKGHTNASIMLFGPGVASE 318
 DB 248 DTR-INSANGLEIKSTEGQSSLTVTNVTTEHYGNVTCVAAANKLGVTNASLVLPFGSVRG 306
 QY 319 VSNGTSRAGCVWLLPLVLL 338
 DB 307 I-NGSISLAVPLWLLAASLL 325

RESULT 5
 US-08-414-657D-41
 Sequence 41, Application US/08414657D
 Patent No. 5861283
 GENERAL INFORMATION:
 APPLICANT: Levitt, Pat
 APPLICANT: Pimenta, Aurea
 APPLICANT: Fischer, Itzhak
 APPLICANT: Zhukareva, Victoria
 TITLE OF INVENTION: Limbic System-Associated Membrane
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION NUMBER:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:

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OM protein - protein search, using sw model

Run on: September 11, 2003, 03:03:33 ; Search time 35 seconds
(without alignments)
415.855 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHSISWIFTGL.....RRAGCVMLLPDLVHLHLKF 344.

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTOS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	926.5	51.3	338	2	US-08-414-657D-42
2	926.5	51.3	338	2	US-08-414-657D-43
3	926.5	51.3	338	4	US-09-135-080-4
4	923.5	51.1	325	2	US-08-414-657D-2
5	923.5	51.1	325	2	US-08-414-657D-41
6	923.5	51.1	325	4	US-09-135-080-2
7	923.5	51.1	338	2	US-08-414-657D-60
8	923.5	51.1	338	4	US-09-135-080-8
9	908	50.3	308	2	US-08-414-657D-46
10	907	50.2	315	2	US-08-414-657D-47
11	905	50.1	310	2	US-08-414-657D-45
12	902	49.9	304	2	US-08-414-657D-44
13	886.5	49.1	287	2	US-08-414-657D-48
14	885.5	49.0	287	2	US-08-414-657D-49
15	796.5	44.1	252	2	US-08-414-657D-56
16	795.5	44.0	252	2	US-08-414-657D-57
17	261	14.5	1395	3	US-09-540-245A-15
18	256	14.2	421	2	US-08-659-984A-1
19	256	14.2	421	3	US-08-660-531-1
20	256	14.2	444	2	US-08-659-984A-5
21	256	14.2	444	3	US-08-660-531-5
22	249.5	13.8	607	2	US-08-752-307B-12
23	249.5	13.8	607	4	US-09-707-802-12
24	249.5	13.8	607	4	US-09-991-326-12
25	246.5	13.6	1018	1	US-08-408-093-6
26	246.5	13.6	1018	1	US-08-408-420A-6
27	246.5	13.6	1018	1	US-08-714-901-6

28	246.5	13.6	1018	3	US-08-040-741-6
29	243.5	13.5	605	2	US-08-752-307B-8
30	243.5	13.5	605	4	US-09-707-802-8
31	243.5	13.5	605	4	US-09-991-326-8
32	243.5	13.5	1018	1	US-08-452-052-2
33	237	13.1	73	2	US-08-414-657D-50
34	237	13.1	73	2	US-08-414-657D-51
35	230.5	12.8	868	1	US-08-374-834-1
36	230.5	12.8	868	2	US-08-644-271-1
37	230.5	12.8	868	4	US-09-077-955-1
38	229.5	12.7	869	1	US-08-374-834-16
39	229.5	12.7	869	2	US-08-644-271-29
40	229.5	12.7	869	4	US-09-077-955-33
41	225.5	12.5	478	5	PCT-US95-08493-15
42	225.5	12.5	868	5	PCT-US95-08493-19
43	225.5	12.5	868	5	PCT-US95-08493-21
44	220.5	12.2	423	4	US-09-778-510-22
45	220.5	12.2	442	4	US-09-778-510-20

ALIGNMENTS

RESULT 1
US-08-414-657D-42
Sequence 42 Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO.: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-414-657D-42

Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 2e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99264333; PubMed-10330412;
 RA Mary A., Strim P., Spaltmann F., Plagge A., Kauselmann G., Buck F.,
 RA Rathjen F.G., Brummendorf T.,
 RT "Neurotactin, A novel neurite outgrowth-promoting Ig-like protein
 RT that interacts with CEP-1 and LAMP-2";
 RL J. Cell Biol. 145:865-876(1999).
 DR EMBL; AJ132998; CAB44445.1;
 DR InterPro: IPR007110; Ig-Like.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS00835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 261 AA; 28205 MW; 80E74DFA658802F3 CRC64;
 Query Match 33.2%; Score 599; DB 13; Length 261;
 Best Local Similarity 52.6%; Pred. No. 1.2e-42;
 Matches 112; Conservative 45; Mismatches 54; Indels 2; Gaps 2;
 QY 11 SISWALFTGLAALCLFQGVPRSGDATPP-KAMDNVTVRGSEATLRCTIDNRVTRVAVL 69
 DB 11 SHWLAANVLGLCLLPAGRLAAGDGFPGAADSLVVRKGDVAVLRVLEGGASKANL 70
 QY 70 NRSTLYAGNKKWGLDPRVLLSNTOYSLIEIQNDVYDEGYTCVOTDNHPTSRVH 129
 DB 71 NRSSIFAGSNWSDVRSIATNRREYSIQDQVDDTDDGPTTCVGTQHTPTMQVH 130
 QY 130 LIVQSPKIVISSDISINEGNISLTCTATGRPEPTVWRHISPRANGFVSEDEYLEIQ 189
 DB 131 LVQVSPKIFRISDIIIVNEGSNVLCLATGKPEPSISWRHISPSAKPFES-GOYLDIY 189
 QY 190 GTRQSGDYECSSANDVAAPVVRVKVTNYP 222
 DB 190 VITRQAGEYECSSANDVSPDVKKVKVTNVP 222
 RESULT 15
 Q8N440 PRELIMINARY; PRT; 226 AA.
 AC Q8N440;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-testis;
 RA Strausberg R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC036771; RAH36771.1;
 DR InterPro: IPR003599; Ig-Like.
 DR InterPro: IPR007110; Ig-Like.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00408; IGC2; 2.
 DR PROSITE: PS00835; IG_LIKE; 2.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 226 AA; 24733 MW; 61EC9E93977B520 CRC64;
 Query Match 30.2%; Score 545.5; DB 4; Length 226;
 Best Local Similarity 49.3%; Pred. No. 3.2e-38;
 Matches 103; Conservative 40; Mismatches 65; Indels 1; Gaps 1;

QY 127 RVHLIVQSPKIVISSDISINEGNISLTCTATGRPEPTVWRHISPRANGFVSEDEYL 186
 DB 2 QVHLTVQVPPKIYDISNDMTVNEGTNVTITCLATGKPEPSISWRHISPSAKPF-ENGQYL 60
 QY 187 EIQITREQSGDYECSSANDVAAPVVRVKVTNYPPISEAKGTGVPVQKGTLOCEAS 246
 DB 61 DIYITRDQAGEYECSSANDVSPDVKKVKVNVNFAPITQEIKSGTVPGRSLIKCEGA 120
 QY 247 AVPSAEQYWKDDKRLIEGKKGVKNRPFELSKLIFFNVSEHDYGNITCVASNKLGHTNA 306
 DB 121 GVPFPAPFYKGEKKLFNGQGGIITQNFSTRSILTVTNVTOEHFNGNTYCAANKLGTNA 180
 QY 307 SIMLFGAGVSEVSGTSRRAGCVWLLPL 335
 DB 181 SLPLNPPTAQYGITGSADVLFCWYLVL 209
 Search completed: September 11, 2003, 03:04:57
 Job time : 82 secs

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Query Match 45.4%; Score 820; DB 4; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-61;
Matches 156; Conservative 62; Mismatches 106; Indels 2; Gaps 2;

QY 11 SISWAFITGLAALCLFQGVPRSGDATFP-KAMDNVTVROGESATLCTIDNRVTRVAVL 69
DB 13 SNQWLAUVLSUCLLPSCLPAGSVDFPFAAVDNNMVRKGTAVLRCLELDGASGAWL 72
QY 70 NRSTILYAGNDKWLCDPRVLLSNTOYQISIEIONVDYDEGPTCSVQTDNHPKTSRVH 129
DB 73 NRSIIIFAGGDKWSVDPRVSLINKROYSLQIONVDYDGGPTCSVQTDNHPKTSRVH 132
QY 130 LIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHSIPKAVGFVSEDEYLEIQ 189
DB 133 LTVQVPPKIYDISNDMTVNEGNTVTLCTATGKPEFFISWRHSIPSAKPF-ENGQYLDIY 191
QY 190 GITRQSGDYECASNDVAAPVVRVRKVTNYPPIYISEAKGTGVPVQKGTQCEASAVP 249
DB 192 GITRQAGYECSAENDVSFDPVRKVVYVNFAPTIQIKSGTVTPGSLRCRCEGAGVP 251
QY 250 SAEFQYKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKLGHNTASIM 309
DB 252 PPAFEWYKGEKFLNGOQIIIONFSTRILATVTVTOEHFEGNVCVAAKNKLGTNASLP 311
QY 310 LFPGGAVSEVSNSTRRAGCVMLLPL 335
DB 312 LNPPSTAQYGITGSADVLFSCWLV 337

RESULT 12
Q8HW98
ID Q8HW98 PRELIMINARY; PRT; 325 AA.
AC Q8HW98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Adult male hypothalamus cDNA, RIKEN full-length enriched library,
DE clone A230106M20 product; weakly similar to limbic system-associated
DE membrane protein precursor (E19s) (CHLAMP, G19-isoform)
DE (Fragment)
DE
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OY NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=2234683; PubMed=12466851;
RA The FANTOM Consortium
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
PT "Analysis of the mouse transcriptome based on functional annotation of
PT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK039193; BAC30273.1;
FT NON-TER
SQ SEQUENCE 325 AA; 35609 MW; F4277BA4A16F707 CRC64;

Query Match 42.0%; Score 759; DB 7; Length 325;
Best Local Similarity 50.3%; Pred. No. 4.4e-56;
Matches 163; Conservative 45; Mismatches 104; Indels 12; Gaps 6;

QY 15 AIFTGALALCLFQGVPRSGDATFPKAMDNVTVROGESATLCTIDNRVTRVAVLNRSTI 74
DB 5 AALAGLAVIS--RG--LLSQSLEFSSPADNVTVCBGDNATLSCFIDEHVTAVLNRNRI 60
QY 75 LYAGNDKWLCDPRVLLSNTOYQISIEIONVDYDEGPTCSVQTDNHPKTSRVH 134
DB 61 LYAGNDKWLCDPRVLLSNTOYQISIEIONVDYDEGPTCSVQTDNHPKTSRVH 120
QY 135 SPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHSIPKAVGFVSEDEYLEIOGTRE 194
DB 121 PARIVNLSFPAVNEGNNVLLCLAVGRPEPTVTVRHSIPKAVGFVSEDEYLEIOGTRE 177

Query Match 38.0%; Score 686.5; DB 11; Length 188;
Best Local Similarity 74.1%; Pred. No. 2.8e-50;
Matches 129; Conservative 18; Mismatches 24; Indels 3; Gaps 1;

QY 12 ISWAFITGLAALCLF---QGVPRSGDATFPKAMDNVTVROGESATLCTIDNRVTRVAV 68
DB 9 LPWKCLVVVSLRLFLVPTGVPVRSQDATFPKAMDNVTVROGESATLCTIDNRVTRVAV 68
QY 69 LNRSTILYAGNDKWLCDPRVLLSNTOYQISIEIONVDYDEGPTCSVQTDNHPKTSRV 128
DB 69 LNRSTILYAGNDKWLCDPRVLLSNTOYQISIEIONVDYDEGPTCSVQTDNHPKTSRV 128
QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHSIPKAVGFVSE 182
DB 129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHSIPKAVGFVSE 182

RESULT 14
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ID Q9W6V1 PRELIMINARY; PRT; 261 AA.
AC Q9W6V1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Neurotactin-S.
DE NTRA-S.
DE
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OY NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC Bruemendorf T.
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Query Match 52.4%; Score 946; DB:7; Length 334;
 Best Local Similarity 55.2%; Pred. No. 6.7e-72;
 Matches 182; Conservative 57; Mismatches 85; Indels 6; Gaps 4;

QY 14 WAIFGTGLAALCLFQGVPRVSGDATFPKAMDNVTYVQGESATLRCTIDNRVTRVAVLNRSST 73
 DB 10 WVL--GFELFLFOGLPVRSD--FTRGTDNITVRQGDAILRCFVEDRSKVAWLNRS 65
 QY 74 ILVAGNDKCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVOTDNHPTKSRVHLVQ 133
 DB 66 IIFAGEDKWSLDPVLEKRSPLYSRLQKVDYDEGPTCSVOTQHPKTSQVYLIQ 125
 QY 134 VSPKIVEISSDISINEGNNISLCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIGITR 193
 DB 126 VPKISNISSDLTVNEGSNVLVCMANGRPVITWRHLTPGKEFEGBEYELIIGITR 185
 QY 194 EOSGDECSASNDVAAPVRRVKVTNYPYISKAGTGVPGVQKGTLOCESAVPSAEF 253
 DB 186 EOSGKECKAANEVASADYKQVTVNYPPTITESKSNEAATGRQALLRCEASAVPTDF 245
 QY 254 QWYKDKRLIEGKGVKVENRPFSLKLIFFENYSEHDYNTCVASNKLGHNTASIMLFGP 313
 DB 246 EWRDTR-INSANGLEIKSGSLSLLVANVTEHYGNYTCVAANKLGVNASLYLRP 304
 QY 314 GAVSEVNSTSRACGCVWLLPLLVHLHLK 343
 DB 305 G-TGRVDNGSVSLAVPLMLLAASLLCLLSK 333.

RESULT 7

Q81V49 PRELIMINARY; PRT; 338 AA.
 AC Q81V49;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to limbic system-associated membrane protein.
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE-Colon;
 RA Strausberg R.;
 PL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC033803; AAH33803.1;
 SQ SEQUENCE 338 AA; 37393 MW; 88CF00E07302817B CRC64;

Query Match 51.6%; Score 932.5; DB:4; Length 338;
 Best Local Similarity 55.4%; Pred. No. 9.5e-71;
 Matches 180; Conservative 60; Mismatches 80; Indels 5; Gaps 4;

QY 20 LAALCLF-OGVPRVSGDATFPKAMDNVTYVQGESATLRCTIDNRVTRVAVLNRSIYAG 78
 DB 17 LRLCLLPGLPVRSD--FNRGTDNITVRQGDAILRCVVEDKSKVAWLNRSIIIFAG 74
 QY 79 NDKWCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVOTDNHPTKSRVHLIVQSPKI 138
 DB 75 HDKWSLDPVLEKRSPLYSRLQKVDYDEGPTCSVOTQHPKTSQVYLIQVPPKI 134
 QY 139 VEISSDISINEGNNISLCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIGITREQSGD 198
 DB 135 SNISSDTVNEGSNVLVCMANGRPVITWRHLTPGKEFEGBEYELIIGITREQSGK 194
 QY 199 YECASNDVAAPVRRVKVTNYPYISKAGTGVPGVQKGTLOCESAVPSAEFQWKD 258
 DB 195 YECKAANEVASADYKQVTVNYPPTITESKSNEAATGRQALLRCEASAVPTDFEYRD 254
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFENYSEHDYNTCVASNKLGHNTASIMLFGVASE 318
 DB 255 DTR-INSANGLEIKSTEGQSLVTVNTEHYGNYTCVAANKLGVNASLYLFRGVRG 313

QY 319 VSNGTSSRACGCVWLLPLLVHLHLK 343
 DB 314 I-NGSISLAVPLMLLAASLLCLLSK 337

RESULT 8
 Q02869 PRELIMINARY; PRT; 350 AA.
 AC Q02869;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CHLAMP, g11-isoform precursor.
 OS Gallus gallus (Chicken)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopteria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=97358596; PubMed=9215692;
 RA Brummendorf T., Spaltmann F., Treubert U.;
 RT Cloning and characterization of a neural cell recognition molecule on
 RT axons of the retinotectal system and spinal cord.;
 RL Eur. J. Neurosci. 9:1105-1116(1997).
 DR EMBL: Z94719; CAB08114.1;
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig-C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00408; IGG2; 2.
 DR PROSITE: PS00835; IG_LIKE; 3.
 KW Brain; GPI-anchor; Immunoglobulin domain; Signal.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 350 CHLAMP, G11-ISOFORM.
 SQ SEQUENCE 350 AA; 38656 MW; 0844A892878894D4 CRC64;

Query Match 51.5%; Score 930.5; DB:7; Length 350;
 Best Local Similarity 54.3%; Pred. No. 1.5e-70;
 Matches 183; Conservative 56; Mismatches 81; Indels 17; Gaps 5;

QY 20 LAALCLF-OGVPRVSGDATFPKAMDNVTYVQGESATLRCTIDNRVTRVAVLNRSIYAG 78
 DB 17 LRLCLLPGLPVRSD--FTRGTDNITVRQGDAILRCFVEDRSKVAWLNRSIIIFAG 74
 QY 79 NDKWCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVOTDNHPTKSRVHLIVQSPKI 138
 DB 75 EDKWSLDPVLEKRSPLYSRLQKVDYDEGPTCSVOTQHPKTSQVYLIQVPPKI 134
 QY 139 VEISSDISINEGNNISLCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIGITREQSGD 198
 DB 135 SNISSDTVNEGSNVLVCMANGRPVITWRHLTPGKEFEGBEYELIIGITREQSGK 194
 QY 199 YECASNDVAAPVRRVKVTNYPYISKAGTGVPGVQKGTLOCESAVPSAEFQWKD 258
 DB 195 YECKAANEVASADYKQVTVNYPPTITESKSNEAATGRQALLRCEASAVPTDFEYRD 254
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFENYSEHDYNTCVASNKLGHNTASIMLFGVASE 311
 DB 255 DTR-INSANGLEIKSTEGQSLVTVNTEHYGNYTCVAANKLGVNASLYLKRVLPTL 313
 QY 312 -----GPAVSEVNSTSRACGCVWLLPLLVHLHLK 343
 DB 314 PNPPFGG-TGRVDNGSVSLAVPLMLLAASLLCLLSK 349

RESULT 9
 Q8BLK3 PRELIMINARY; PRT; 341 AA.
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DE CPU-SE alpha 1 isoform.
GN CPU-SE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RT "Characterisation of CPU-SE, a secreted isoform of the IgLON family protein CEPU-1".
RL EMBL: AF292936; AAG01879.1; -
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00408; Igc2; 2.
DR PROSITE: PS0835; IG-LIKE; 3.
ZW Immunoglobulin domain.
SQ SEQUENCE 313 AA; 34606 MW; 68C5D27FDDC6FB2 CRC64;

Query Match 75.2%; Score 1357.5; DB 13; Length 315;
Best Local Similarity 83.0%; Pred. No. 8.5e-107;
Matches 253; Conservative 26; Mismatches 23; Indels 3; Gaps 1;
QY 11 STSWAIFGLAALCLF---OGVPVRSQDTPPKAMDNVTVROGESATLRCITDNRVTRVA 67
DB 8 LPWCLVVLCLRLLELVPAGVPVRSQDTPPKAMDNVTVROGESATLRCITDNRVTRVA 67
QY 68 WLNRSILYAGNDKWLDPRLVLLSNTQTSYISIQNVYDDEGPTCVQVDNHPKTSR 127
DB 68 WLNRSILYAGNDKWLDPRLVLLANTQYISIQHVDYDEGPTCVQVDNHPKTSR 127
QY 128 VHLIVQSPKIVEISSDISINEGNISLTCTATGPRPTVTRHISPKAVGVSEDEYLE 187
DB 128 VHLIVQSPKIVEISSDISINEGNISLTCTATGPRPTVTRHISPKAVGVSEDEYLE 187
QY 188 IGGITREOSGDEYECASNDVAAPVRRVKVTNPPYISAKGTGVPVQKGTQCEASA 247
DB 188 ITGITREOSGDEYECASNDVAAPVRRVKVTNPPYISAKGTGVPVQKGTQCEASA 247
QY 248 VPSAEFQYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 307
DB 248 VPSAEFQYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 307
QY 308 IMLFG 312
DB 308 MILYG 312

RESULT 5
ID Q9DF61 PRELIMINARY; PRT: 344 AA.
JC 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE OBCAM alpha 1 isoform.
GN OBCAM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Lodge A.P., Howard M.R., McNamee C.J., Moss D.J.;
RT "Co-localisation, heterophilic interactions and regulated expression"

RT of IgLON family proteins in the chick nervous system.";
RL Brain Res. Mol. Brain Res. 82:84-94(2000).
DR EMBL: AF292934; AAG01877.1; -
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00408; Igc2; 2.
DR PROSITE: PS0835; IG-LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 344 AA; 37531 MW; 37FE6051CBF0E7B4 CRC64;
Query Match 70.6%; Score 1275.5; DB 13; Length 344;
Best Local Similarity 72.8%; Pred. No. 8.5e-100;
Matches 246; Conservative 32; Mismatches 53; Indels 7; Gaps 3;
QY 12 ISWAIFGLAALCLF---OGVPVRSQDTPPKAMDNVTVROGESATLRCITDNRVTRVA 68
DB 9 LPWCLVVLCLRLLELVPAGVPVRSQDTPPKAMDNVTVROGESATLRCITDNRVTRVA 68
QY 69 WLNRSILYAGNDKWLDPRLVLLSNTQTSYISIQNVYDDEGPTCVQVDNHPKTSR 128
DB 69 WLNRSILYAGNDKWLDPRLVLLSNTQTSYISIQNVYDDEGPTCVQVDNHPKTSR 128
QY 129 HLIQVSPKIVEISSDISINEGNISLTCTATGPRPTVTRHISPKAVGVSEDEYLE 188
DB 129 HLIQVSPKIVEISSDISINEGNISLTCTATGPRPTVTRHISPKAVGVSEDEYLE 188
QY 189 OGITREOSGDEYECASNDVAAPVRRVKVTNPPYISAKGTGVPVQKGTQCEASA 248
DB 189 TGITREOSGDEYECASNDVAAPVRRVKVTNPPYISAKGTGVPVQKGTQCEASA 248
QY 249 PSAEFQYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 308
DB 249 PSAEFQYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 308
QY 309 MLFGGAVSEVSGTSSRRAG--CVMLPLLVLLHLLKF 344
DB 309 ILYGPGAVHDSGNAASRAAGICLW--ATLLARLLDF 344
RESULT 6
ID 002870 PRELIMINARY; PRT: 334 AA.
JC 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE CHAMP g9-isoform precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Brummendorf T., Spaltmann F., Treubert U.;
RT "Cloning and characterization of a neural cell recognition molecule on axons of the retinotectal system and spinal cord.";
RL Eur. J. Neurosci. 9:1105-1116(1997).
DR EMBL: Z94718; CAB08113.1; -
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00408; Igc2; 2.
DR PROSITE: PS0835; IG-LIKE; 3.
KW Brain; GPI-anchor; Immunoglobulin domain; Signal.
FT SIGNAL 1 24 POTENTIAL
FT CHAIN 25 334 CHLAMP, G9-ISOFORM
SQ SEQUENCE 334 AA; 37288 MW; 0B40A768D9609E77 CRC64;

Thu Sep 11 16:21:01 2003

us-10-017-084a-523.rspt

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Db 121 NHPKTSRVHLVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGV 180
QY 181 SEDYLEIQITREQSGDYECASNDVAAPVVRKVTVNPPYISAKGTGVPVGOKT 240
Db 181 SEDYLEIQITREQSGDYECASNDVAAPVVRKVTVNPPYISAKGTGVPVGOKT 240
QY 241 LQCSASVPSAEQWYKDKKRLIEGKGVKVENRPLSKLIFNFVSEHDYGNVTCVSNK 300
Db 241 LQCSASVPSAEQWYKDKKRLIEGKGVKVENRPLSKLIFNFVSEHDYGNVTCVSNK 300
QY 301 LGHTNASIMLFGGAVSEVNGTSRRAGCVWLLPLLVHLLKLF 344
Db 301 LGHTNASIMLFGGAVSEVNGTSRRAGCVWLLPLLVHLLKLF 344

RESULT 2
O57596
ID O57596 PRELIMINARY; PRT; 313 AA.
AC O57596;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE Neural secreted glycoprotein (CEPU-SE alpha 2 isoform).
GN CEPU OR CEPU-SE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim D., Moss D.J.;
RT Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
RL [2]
RW TISSUE=Brain;
RC Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RT "Characterisation of CEPU-Se, a secreted isoform of the IgLON family protein CEPU-1."
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ225897; CAAL2649.1;
DR EMBL; AF292935; AAG01878.1;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; Igc2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 313 AA; 34482 MW; 99AD825CAB4A5347 CRC64;

Query Match 79.18; Score 1428; DB 13; Length 313;
Best Local Similarity 85.48; Pred. No. 9e-113;
Matches 263; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 5 QPKWHSISWAFITGLAALCLFQGVPRSGDATFPKAMDNVTRQESATLRCITDNRVT 64
Db 3 QAKQHPVSVWIFAGWALLLFQGVPRSGDATFPKAMDNVTRQESATLRCITDNRVT 62
QY 65 RVAMLNRSTLYAGNDKWCIDPRVLLSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPK 124
Db 63 RVAMLNRSTLYAGNDKWCIDPRVLLSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPK 122
QY 125 TSVRHVLIQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDE 184
Db 123 TSVRHVLIQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDE 182
QY 185 YLEIQITREQSGDYECASNDVAAPVVRKVTVNPPYISAKGTGVPVGOKTQCE 244
Db 183 YLEITGITREQSGDYECASNDVAAPVVRKVTVNPPYISAKGTGVPVGOKILMCE 242
QY 245 ASAVPSAEQWYKDKKRLIEGKGVKVENRPLSKLIFNFVSEHDYGNVTCVSNKLGHT 304
Db 245 ASAVPSAEQWYKDKKRLIEGKGVKVENRPLSKLIFNFVSEHDYGNVTCVSNKLGHT 304
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Db 243 ASAVPSAEQWYKDKKRLAEQKGLKVENKAFKSLRTFFNVSEQDYGNVTCVAS 180
QY 305 NASIMLFG 312
Db 303 NASMILYG 310

RESULT 3
O93242
ID O93242 PRELIMINARY; PRT; 344 AA.
AC O93242;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CEPU-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.;
RT "CEPU-1: an immunoglobulin Superfamily Molecule, Has Cell Adhesion Activity and Shows Dynamic Expression Patterns in Chick Embryonic Spinal Cord."
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB011810; BAA31514.1;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; Igc2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 344 AA; 37613 MW; 22CAA8F526A6B57E CRC64;

Query Match 79.08; Score 1427.5; DB 13; Length 344;
Best Local Similarity 79.28; Pred. No. 1.e-112;
Matches 267; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 11 SISWAFITGLAALCLF---QGVPRSGDATFPKAMDNVTRQESATLRCITDNRVTRVA 67
Db 8 ALPWRCLVLCRLLELVPAGVPVSGDRTFPKAMDNVTRQESATLRCITDNRVTRVA 67
QY 68 WLNRSITLYAGNDKWCIDPRVLLSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPKTSR 127
Db 68 WLNRSITLYAGNDKWCIDPRVLLSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPKTSR 127
QY 128 VHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLE 187
Db 128 VHLIVQVSPKITEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLE 187
QY 188 IGTITREQSGDYECASNDVAAPVVRKVTVNPPYISAKGTGVPVGOKTQCEASA 247
Db 188 IGTITREQSGDYECASNDVAAPVVRKVTVNPPYISAKGTGVPVGOKILMCEASA 247
QY 248 VPSAEQWYKDKKRLIEGKGVKVENRPLSKLIFNFVSEHDYGNVTCVSNKLGHTNAS 307
Db 248 VPSAEQWYKDKKRLAEQKGLKVENKAFKSLRTFFNVSEQDYGNVTCVSNKLGHTNAS 307
QY 308 IMLPGCAVSEVNGTSRRAGCVWLLPLLVHLLKLF 344
Db 308 IMLPGCAVHDGNSGAWRSGCAMLALPLAQLAROF 344

RESULT 4
O9DG15
ID O9DG15 PRELIMINARY; PRT; 315 AA.
AC O9DG15;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
```

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OM protein - protein search, using sw model

Run on: September 11, 2003, 03:01:28 ; Search time 78 seconds
(without alignments)
1138.078 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 1806

Sequence: 1 MKTIQPKMHSISWAIFTGL.....RRAGCVMLPLLVLLHLLKF 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_ricent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1780	98.6	344	11 Q8BG33	Q8BG33 mus musculus
2	1428	79.1	313	13 Q57596	Q57596 gallus gall
3	1427.5	79.0	344	13 Q93242	Q93242 gallus gall
4	1357.5	75.2	315	13 Q9DG15	Q9DG15 gallus gall
5	1275.5	70.6	344	13 Q9DF61	Q9DF61 gallus gall
6	945	52.4	334	7 Q02870	Q02870 gallus gall
7	932.5	51.6	338	4 Q8IV49	Q8IV49 homo sapien
8	930.5	51.5	350	7 Q02869	Q02869 gallus gall
9	894	49.5	341	11 Q8BLK3	Q8BLK3 mus musculus
10	842	45.6	352	13 Q9W6V2	Q9W6V2 gallus gall
11	820	45.4	325	4 Q8NAQ3	Q8NAQ3 homo sapien
12	759	42.0	325	7 Q8HW98	Q8HW98 mus musculus
13	686.5	38.0	188	11 Q8BWT5	Q8BWT5 mus musculus
14	599	33.2	261	13 Q9W6V1	Q9W6V1 gallus gall
15	545.5	30.2	226	4 Q8N440	Q8N440 homo sapien
16	380.5	21.1	606	5 Q9VMN6	Q9VMN6 drosophila

17	350.5	19.4	672	5 Q8IP70	Q8IP70 drosophila
18	348	19.3	554	5 Q9W4K3	Q9W4K3 drosophila
19	338.5	18.7	413	5 Q9VAR6	Q9VAR6 drosophila
20	333	18.4	315	5 Q9VMB2	Q9VMB2 drosophila
21	308.5	17.1	528	5 P91670	P91670 drosophila
22	306	16.9	545	5 Q9VCT4	Q9VCT4 drosophila
23	303.5	16.8	316	5 Q8WP83	Q8WP83 drosophila
24	301	16.7	526	5 Q9VMN9	Q9VMN9 drosophila
25	300.5	16.6	316	5 Q8WP94	Q8WP94 drosophila
26	297.5	16.5	316	5 Q8WP58	Q8WP58 drosophila
27	290.5	16.1	2673	4 Q9GSC3	Q9GSC3 homo sapien
28	290.5	16.1	5636	4 Q9ERW7	Q9ERW7 homo sapien
29	287	15.9	846	13 Q57577	Q57577 cynops pyrr
30	287	15.9	1100	13 Q57576	Q57576 cynops pyrr
31	285.5	15.8	373	5 Q9VLF0	Q9VLF0 drosophila
32	285.5	15.8	603	5 Q9NKF5	Q9NKF5 drosophila
33	284	15.7	403	5 Q9VP08	Q9VP08 drosophila
34	282.5	15.6	605	11 Q921P2	Q921P2 mus musculus
35	282.5	15.6	838	11 Q8C4B2	Q8C4B2 mus musculus
36	282.5	15.6	838	11 Q8B096	Q8B096 mus musculus
37	279.5	15.5	725	13 Q73633	Q73633 xenopus lae
38	278.5	15.4	4162	13 Q98918	Q98918 gallus gall
39	273.5	15.1	725	13 Q73634	Q73634 xenopus lae
40	272.5	15.1	1323	13 Q8A476	Q8A476 gallus gall
41	269.5	14.9	484	5 Q54475	Q54475 schistocerc
42	268.5	14.9	1456	5 Q92626	Q92626 homo sapien
43	265	14.7	1482	5 Q9V4Y0	Q9V4Y0 drosophila
44	261.5	14.5	437	4 Q8IZP8	Q8IZP8 homo sapien
45	261	14.5	1031	13 Q90VM2	Q90VM2 brachydanio

ALIGNMENTS

RESULT 1

Q8BG33 PRELIMINARY: PRT: 344 AA.
AC Q8BG33;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Neurotrophin precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA the FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002)
DR ENBL; AK045973; BAC32555.1;
DR ENBL; AK046377; BAC32695.1;
SQ SEQUENCE 344 AA: 37941 MW: CDA5299D4CD86065 CRC64

Query Match 98.6%; Score 1780; DB 11; Lf
Best Local Similarity: 98.0%; Pred. No. 1.6e-142;
Matches 337; Conservative 5; Mismatches 2;

QY 1 MKTIQPKMHSISWAIFTGLAALCLFQGVPRVSRSDATFPK
Db 1 MKTIQPKMHSISWAIFTGLAALCLFQGVPRVSRSDATFPK
QY 61 NRVTFAWLNRSITLYAGNDKWCIDPRVLLSNTOFO
Db 61 NRVTFAWLNRSITLYAGNDKWCIDPRVLLSNTOFO
QY 121 NHPTKSRVHLIVQVSPKIVETSSDISINEGNNIS?
Db 121 NHPTKSRVHLIVQVSPKIVETSSDISINEGNNIS?

Page 2

Page 2

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FT DISULFID 139 189 PROBABLE.
FT DISULFID 235 288 PROBABLE.
FT DISULFID 330 386 PROBABLE.
FT DISULFID 427 480 PROBABLE.
FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 479 479 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 810 1076 Missing (in isoform N-CAM 140).
FT VARSPLIC 810 1076 /FTIG-VSP_002588.
SQ SEQUENCE 1115 AA; 119351 MW; 2C93DCD474CFBCAF CRC64;

Query Match 15.7%; Score 283.5; DB 1; Length 1115;
Best Local Similarity 25.8%; Pred. No. 1.6e-14;
Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

QY 44 NVTVRQGESATLRCTIDNRVTRVAMLRSTILYAGNDKWCCLDPVV-----LLSNTQ 95
DB 222 NATANLGQSVTLVCDAG-----PPEPTM-----SWTKDGEPIENEEDERSRSVS 268

QY 96 TOYSTEIONVDYDEGPTCTGVTQDNHPTKSRVHLIVQSPKIVEISSDISINEGNISL 155
DB 269 DSSEVTIRNVKNDDEAYVCIAENKAGEODASIHVKFAPKITYVENQTAMELEEQVTL 328

QY 156 TCIATGREPTVTR-----HISPKAVGFVSEDEYLEIOGITRQSGDYE 200
DB 329 TEASGDPIPSITWRTSTNRNISSEODLDGHVVRSHRVSS---LTLASIQYRDAGEYM 385

QY 201 CSASNDVAAPVVRVKVTVNPPYISEAKGTGVPVGOKGLQCEASAVPSAEFYWKDDK 260
DB 386 CRASNTIGQD-SQSIDLEFOYAPKIQGVPVYTWEGNQVNIICEVAYPSATISWFRDQG 444

QY 261 RLIEGK-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNLGHTNASIML 310
DB 445 LLPSSNYSNIKIYNTPSASYLEVTDPDENFGYNCTAVNVRIGOSLEFIL 495

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Search completed: September 11, 2003, 03:03:27
Job time : 36 secs

Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

QY 44 NVVROGESATLRCIDNRVTRVAVLNRSTLYAGNDKWCIDPRV-----LLSWTO 95
 Db 222 NATANLQSVTLVCDAG-----PFETM-----SWTKDGPENEDERSSVS 268
 QY 96 TOYSEIQNVYDEGPYTCVQDNHPTKTSRVHLIVQSPKIVSEISSIDISNEGNISL 155
 Db 269 DSEVTIRNVNDKAEAYVCIENKAGEQDASHLKVFAKPKITYVENQTAMELEEQVTL 328
 QY 156 TCIATGRPEPTVWR-----HISPKAVGFVSEDEYLEIGITREOSGDYE 200
 Db 329 TCASGDGPIPTWRTSTRNISSEODLDGHMVVSHARVSS---LTLKSIQYRDAGYM 385
 QY 201 CSASNDVAAPVVRVRYVNVYPIYSEAKGTGVPVQKGTLCQCEASAVPSAEFOYKDDK 260
 Db 386 CTASNTIGOD-SQSIDLEFOYAPKLAGPVAVYTWEQNVNITCEVAYPSATISWFRDQ 444
 QY 261 RLIEGR-KGVKVENRPFSLKIFNVSEHDYGNVTCVASKNLGHTNASIML 310
 Db 445 LLPSSNYSNIKIYNTPSASYLEVTPDSEDFGNCVAVNIGTAVNRIGOSLEFIL 495

RESULT 15

NCAM_MOUSE STANDARD; PRT; 1115 AA.

AC P13525; 061949;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180)
 DE (NCAM-180)
 GS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM N-CAM 180).
 RC STRAIN=C57BL/6;
 RX MEDLINE=87246524; PubMed=3595563;
 RA Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C.,
 RA Hirsch M.R., Fontecilla-Camps J.C., Goridis C.;
 RT "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
 RT a Mr 79,000 polypeptide without a membrane-spanning region.";
 RL EMBO J. 5:907-914(1987).
 RN [2]
 RP SEQUENCE OF 529-1115 FROM N.A. (ISOFORM N-CAM 140).
 RC STRAIN=C57BL/6;
 RX MEDLINE=88057687; PubMed=3684567;
 RA Santoni M.-J., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M.,
 RA Goridis C., Wille W.;
 RT "Analysis of cDNA clones that code for the transmembrane forms of the
 RT mouse neural cell adhesion molecule (NCAM) and are generated by
 RT alternative RNA splicing.";
 RL Nucleic Acids Res. 15:8621-8641(1987).
 RN [3]
 RP SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180).
 RX MEDLINE=98203628; PubMed=3396534;
 RA Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
 RT "Differential splicing and alternative polyadenylation generates
 RT distinct NCAM transcripts and proteins in the mouse.";
 RL EMBO J. 7:625-632(1988).
 RN [4]
 RP SEQUENCE OF 804-1081 FROM N.A. (ISOFORM N-CAM 180).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=88247737; PubMed=2454455;
 RA Barthels D., Vopper G., Wille W.;
 RT "NCAM-180, the large isoform of the neural cell adhesion molecule of
 RT the mouse, is encoded by an alternatively spliced transcript.";
 RL Nucleic Acids Res. 16:4217-4225(1988).
 RN [5]
 RP SEQUENCE OF 702-1115 FROM N.A. (ISOFORM N-CAM 140).

RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=89251563; PubMed=2711486;
 RA Santoni M.-J., Barthels D., Vopper G., Boned A., Goridis C., Wille W.;
 RT "Differential exon usage involving an unusual splicing mechanism
 RT generates at least eight types of NCAM cDNA in mouse brain.";
 RL EMBO J. 8:385-392(1989).
 RN [6]
 RP SEQUENCE OF 20-36.
 RX MEDLINE=86140120; PubMed=3512556;
 RA Rougon G., Marshak D.R.;
 RT "Structural and immunological characterization of the amino-terminal
 RT domain of mammalian neural cell adhesion molecules.";
 RL J. Biol. Chem. 261:3396-3401(1986).
 CC -I- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=N-CAM 180;
 CC IsoId=PI3595-1; Sequence=Displayed;
 CC Name=N-CAM 140;
 CC IsoId=PI3595-2; Sequence=VSP_002588;
 CC Name=N-CAM 120;
 CC IsoId=PI3594-1; Sequence=External;
 CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -I- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -I- SIMILARITY: Contains 2 fibronectin type III domains.
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 CC -----
 CC EMBL: X07200; CAA30177.1;
 CC EMBL: Y00051; -; NOT_ANNOTATED_CDS.
 CC EMBL: X06328; CAA29641.1;
 CC EMBL: X07195; CAA30173.1;
 CC EMBL: X07244; CAA30230.1;
 CC EMBL: X15051; CAA33150.1;
 CC EMBL: X15052; CAA33151.1;
 CC PIR: A29673; IJMSNL.
 CC MGD: MGI:97281; Ncam1.
 CC InterPro: IPR003961; FN-III.
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003598; Ig_C2.
 CC InterPro: IPR003006; Ig_MHC.
 CC Pfam: PF00041; fn3_2.
 CC Pfam: PF00047; fn3_5.
 CC SMART: SM00060; FN3_2.
 CC SMART: SM00408; IGC2; 5.
 CC PROSITE: PS50835; Ig-Like; 5.
 CC Cell adhesion; glycoprotein; Transmembrane; Repeat;
 CC immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.
 CC SIGNAL 1 19
 CC CHAIN 20 1115 NEURAL CELL ADHESION MOLECULE 1, 180 kDa
 CC ISOFORM.
 CC DOMAIN 20 711 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 712 729 POTENTIAL.
 CC DOMAIN 730 1115 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 116 205 IG-LIKE C2-TYPE 1.
 CC DOMAIN 212 302 IG-LIKE C2-TYPE 2.
 CC DOMAIN 309 402 IG-LIKE C2-TYPE 3.
 CC DOMAIN 407 492 IG-LIKE C2-TYPE 4.
 CC DOMAIN 519 596 IG-LIKE C2-TYPE 5.
 CC DOMAIN 625 692 FIBRONECTIN TYPE-III 1.
 CC DOMAIN 152 156 FIBRONECTIN TYPE-III 2.
 CC DOMAIN 161 165 HEPARIN-BINDING (POTENTIAL).
 CC DISULFID 41 96 HEPARIN-BINDING (POTENTIAL).
 CC PROBABLE.

QY 68 WLNSTILVAGNDKWCLEDRVLLSNTOTQYSTEIONVDVYDEGPTCSVOTDNIHKTSR 127
 DB 65 WLNRSIIIFAGGDKWSDVPSVSLTNLKNRYSLOQYONVDVYDDGPTCSVOTHTPTMQ 124
 QY 128 VHLIVQSPKIVEISSDISINEGNSISLCTIATGPETPTVWRHISPAKVGVSEDEYLE 187
 DB 125 VHLTVQVPPKIIYDISNDMTINEGTNTVLTCLATGPPEPAISWRHISESAKPP-ENGQYLD 183
 QY 188 IOGTIRQSGDCEASNDVAAPVVRVKVTVNYPPYISEAKGTVGVGKGKGTLOCEASA 247
 DB 184 IYGTIRDOAGEYCEASNDVSFPDVKRVVNVNFAPTIOETKSGTVTPGKSLRCEGAG 243
 QY 248 VPSAEQFWKDKDRLEIEKGKVKVNRPELSKLIFFENYSEHDYNTCYVASKLGHNTAS 307
 DB 244 VPPPAPEWKGEKRLFNQOQIIIFNSTRSILTVNTVQEHFNGVTCVAAKLGTTNAS 303
 QY 308 IMIFGPGAVSEVSNSTRAGCVMLPLVLLHLKLF 344
 DB 304 LPLNPPSTAYQITGSCADLFSCWSLALTLSVISIF 340

RESULT 13
 ID AMAL DROME STANDARD; PRT; 333 AA.
 AC P15164; 09V3A5;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amalgam protein precursor.
 GN AMA OR BG:DS00276.6 OR CG2198.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=99028670; PubMed=3141062;
 RA Seeger M.A., Haifley L., Kaufman T.C.;
 RT "Characterization of amalgam: a member of the immunoglobulin
 superfamily from Drosophila."
 RL Cell 55:589-600(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RA Palazzolo M.J.;
 RT "Complete sequence of the Antennapedia complex of Drosophila."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides F.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA Sutton R.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Watanabe K., Rogers J.H., Blazer R.G., Chao M., Pfeiffer B.D.,
 RA Brandon R.C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA DeDonato K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA DeBin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
 RA Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Harris N.L., Harvey D., Heiman T.J., Gu Z., Guan P., Harris M.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattle B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Mishina N.V., Mobarry C., Morris J., Moharefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert-K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Williams S.M., Woodage D.A., Weinstein G.M., Weissbach J.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely; TISSUE=Embryo;
 EX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Wan K.H.,
 RA George R.A., Guarini H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.W., Celniker S.E.;
 RT "A Drosophila full-length cDNA resource."
 RL Genome Biol. 3:RESEARCH0080.11-RESEARCH0080.8(2002).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
 (POSSIBLE).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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 or send an email to license@isb-sib.ch).
 DR EMBL; M23561; AAA28367.1;
 DR EMBL; AE001572; AAD19797.1;
 DR EMBL; AE003674; AAF54084.1;
 DR EMBL; AY051911; AAK93335.1;
 DR PIR; A31923; A31923.
 DR FlyBase; FBgn0000071; Ama.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003006; Ig_WHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGG2; 2.
 DR PROSITE; PS50833; IG_LIKE; 3.
 KW Immunoglobulin domain; Glycoprotein; GPI-anchor; Signal; Repeat.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 ? ? ANALAM PROTEIN.
 FT PROPEP 25 333 REMOVED IN MATURE FORM (POTENTIAL).
 FT DOMAIN 139 228 IG-LIKE V-TYPE.
 FT DOMAIN 139 228 IG-LIKE C2-TYPE 1.
 FT DOMAIN 230 323 IG-LIKE C2-TYPE 2.
 FT DISULFID 46 117 PROBABLE.
 FT DISULFID 161 208 PROBABLE.
 FT DISULFID 251 307 PROBABLE.
 FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 83 83 O -> K (IN REF. 1).
 SQ SEQUENCE 333 AA; 36387 MW; F644753DE3DB25F1 CRC64;

Query Match
 Best Local Similarity 16.5%; Score 297 5; DB 1; Length 333;
 Matches 87; Conservative 43; Mismatches 136; Indels 27; Gaps 11;

CC DETECTED IN PRESUMPTIVE CORTEX, MEDIAL LIMBIC AREAS OF THE
CC THALAMUS AND HYPOTHALAMUS. IN THE ADULT, IT IS FOUND IN
CC HIPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC
CC REGION.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U31554; AAA86120.1; -
CC InterPro: IPR007110; IG-LIKE.
CC InterPro: IPR003598; IG_C2.
CC Pfam: PF00047; IG_3.
CC SMART: SM00408; IGC2; 2.
CC PROSITE: PS50835; IG-LIKE; 3.
CC Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
CC Repeat; Signal 1 28
CC CHAIN 29 315
CC
CC LIMBIC SYSTEM-ASSOCIATED MEMBRANE
CC PROTEIN. IN MATURE FORM (POTENTIAL).
CC IG-LIKE C2-TYPE 1.
CC IG-LIKE C2-TYPE 2.
CC IG-LIKE C2-TYPE 3.
CC POTENTIAL.
CC POTENTIAL.
CC POTENTIAL.
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC GPI-ANCHOR (POTENTIAL).
CC SEQUENCE 338 AA; 37324 MW; 0B76AFDD68A39BB6.CRC64;

Query Match 51.3%; Score 926.5; DB 1; Length 338;
Best Local Similarity 55.1%; Pred. No. 4.2e-66;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;
OY 20 LAALCLF-OGVPRVSGDATFPKAMDNVTYVROGESATLRCITDNRVTRVWLNSTLYAG 78
DB 17 LRLCLLPTGLPVRSD--FNRGTDNITVROGDTAILRCVVDKNSKVWLNRSGLIF 74
OY 79 NDKXCLDPRVLLSNTQYSEIQNVYDDEGPTCSQVTDNHPKTSRVLLIVQVSPKI 138
DB 75 HDKSLDPRVELEKHALEYSLRIQKVDYDEGPTCSQVQHEPKTSQVLLIVQVPKI 134
OY 139 VEISSDISINENNNISLTCIATGRPEPTVTHRIHSPKAVGVFSDEYLETQGITRQSGD 198
DB 135 SNISSDVTYNEGSNTVLCMANGREPEVITWRHLPLGREFEGEEYLELITRQSGK 194
OY 199 YECASNDVAAPVVRVVRVTYVYPISEAKGTGVVQKGTQCEASAYPSAEFQWKD 258
DB 195 YECKAANEVSSADVQKRVTVNYPPTITESKNEATGTQASLKCEASAVPAPDFEWYRD 254
OY 259 DKRLIEKGVKVENRPFLLKLIFFNVSEHDYNTYCVASNKLGHTNATLMPGPGAYSE 318
DB 255 DTR-INSANGLEIKSTEGQSSLTNTVTEHYGNTYCVAAANKLGVTNATSLVLPFGSVRG 313
OY 319 VSGTSSRACGVWLLPLLVHLHLK 343
DB 314 I-NGSISLAVPLWLLAASFLCLSK 337

RESULT 12
KILON_RAT
ID KILON_RAT STANDARD; PRT; 348 AA.
AC Q9Z0J8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Kilon protein precursor. (Kindred of IGLON).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-62.
RX MEDLINE=99175207; PubMed=10075727;
RA Funatsu N., Miyata S., Kumanogoh H., Shigeta M., Hamada K., Endo Y.,
RA Sokawa Y., Maekawa S.;
RT "Characterization of a novel rat brain glycosylphosphatidylinositol-
anchored protein (Kilon), a member of the IGLON cell adhesion molecule
family".
RL J. Biol. Chem. 274:8224-8230(1999).
CC -1- FUNCTION: CELL-ADHESION (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Highly expressed in brain.
CC -1- PTM: GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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CC
CC EMBL; AB017139; BA075649.1;
CC InterPro: IPR007110; IG-LIKE.
CC InterPro: IPR003598; IG_C2.
CC InterPro: IPR003006; IG_MHC.
CC Pfam: PF00047; IG_3.
CC SMART: SM00408; IGC2; 2.
CC PROSITE: PS50835; IG-LIKE; 3.
CC Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
CC Repeat; Signal 1 31
CC CHAIN 32 317
CC PROPEP 32 348
CC DOMAIN 32 128
CC DOMAIN 133 215
CC DOMAIN 219 307
CC DISULFID 34 112
CC DISULFID 134 197
CC DISULFID 239 291
CC CARBOHYD 67 67
CC CARBOHYD 149 149
CC CARBOHYD 259 269
CC CARBOHYD 280 280
CC CARBOHYD 288 288
CC CARBOHYD 301 301
CC SEQUENCE 348 AA; 37858 MW; 37E90D1C7D2ACAB.CRC64;
Query Match 45.1%; Score 815; DB 1; Length 348;
Best Local Similarity 47.5%; Pred. No. 2.9e-57;
Matches 160; Conservative 66; Mismatches 101; Indels 10; Gaps 5;

OY 11 STSW--AFTGLAALCLFQGVPRVSGDATFP-KAMDNVTYVROGESATLRCITDNRVTRVA 67
DB 11 SNQWLAAYVLLSCLSC-CLPAGQSV-----DFFPAADVMDMLYRKGDVAVLECYLEDGASKGA 64

Db 195 YECCAANEVASADVKQVTVNYPTTESKSNKNEATGQALLRCEASAVPPDFEWYRD 254
 QY 259 DKRLIEGKGVAVENRPFSLIFENVSEHDYGNVTCVASKNKLGHNTSMIFGPGAVSE 318
 Db 255 DTR-INSANGLEIKSTGQSLLVMANVTEEHGNTVCAANKLGVTNLSLYLRG-TGR 312
 QY 319 VSGTSTRACGVLLPLVLLHLK 343
 Db 313 VDNGSVSLAVPLMLLAASLLCLSK 337

RESULT 10

LAMP HUMAN STANDARD; PRT; 338 AA.
 AC Q13449
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Limbic system-associated membrane protein precursor (LSAMP).
 GN LSAMP OR LAMP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=96235133; PubMed=8666243;
 RA Pimenta A.F., Fischer I., Levitt P.;
 RT "cDNA cloning and structural analysis of the human limbic-system-
 associated membrane protein (LAMP).";
 RL Gene 170:189-195(1996).
 CC -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
 CC CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
 CC OF THE HYPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON LIMBIC NEURONS AND FIBER TRACIS
 CC AS WELL AS IN SINGLE LAYERS OF THE SUPERIOR COLLICULUS, SPINAL
 CC CHORD AND CEREBELLUM.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
 CC SUBFAMILY.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U41901; AAC50569.1;
 CC PIR; JC4776; JC4776.
 CC Genew; HGNC:6705; LSAMP.
 CC MIM; 603241;
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003598; IG-C2.
 CC InterPro; IPR003006; IG_MHC.
 CC Pfam; PF00047; IG; 3.
 CC SMART; SW00408; IGC2; 2.
 CC PROSITE; PS00835; IG-Like; 3.
 CC Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 CC Repeat; Signal.
 CC SIGNAL 1 28
 CC CHAIN 29 315
 CC PROPEP 316 338
 CC DOMAIN 29 122
 CC DOMAIN 132 214
 CC DOMAIN 219 304
 CC DISULFID 53 111
 CC POTENTIAL.
 CC LIMBIC SYSTEM-ASSOCIATED MEMBRANE
 CC PROTEIN.
 CC REMOVED IN MATURE FORM (POTENTIAL).
 CC IG-LIKE C2-TYPE 1.
 CC IG-LIKE C2-TYPE 2.
 CC IG-LIKE C2-TYPE 3.
 CC POTENTIAL.

FT DISULFID 153 197 POTENTIAL..
 FT DTSLFID 239 290 POTENTIAL..
 FT CARBOHYD 40 40 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 148 148 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 279 279 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC..) (POTENTIAL).
 FT LIPID 315 315 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 338 AA; 37308 MW; 0345F2F6DF5D92F CRC64;
 Query Match 51.6%; Score 931.5; DB 1; Length 338;
 Best Local Similarity 55.4%; Pred. No. 1.7e-66;
 Matches 180; Conservative 60; Mismatches 80; Indels 5; Gaps 4;
 QY 20 LAALCLF-QGVPRSGDATPKAMDNVTVROGESATLRCTIDNRVTRVAMLRSTLYAG 78
 Db 17 LELLCLEPTGLPVRSD--FNRGTDITVROGDTAILRCLVEDKSKVAMLRSGIIFAG 74
 QY 79 NDKWCLDRVYLLSNTQTOYSIEIQNVVDYDEGYTCVSQTDNHPKTSRVLHIVQVSPKI 138
 Db 75 HDKWSLDPRVELEKRHSLEYSRLQKVDYDEGYTCVSQTOHEPKTSQVTLIVQVPPKI 134
 QY 139 VEISSDISINEGNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEIOGITREGSD 198
 Db 135 SNISSDVTVNEGSNVTLCMANGREPEVITWHLTPGTGREGEEYLEILGITREGSGK 194
 QY 199 YECASNDVAPVVRVVKVTVNYPYISEAKGTGVPVGOKGTLOCEASAVSASFQYKD 258
 Db 195 YECCAANEVSADVKQVTVNYPTTESKSNKNEATGQALLRCEASAVPPDFEWYRD 254
 QY 259 DKRLIEGKGVAVENRPFSLIFENVSEHDYGNVTCVASKNKLGHNTSMIFGPGAVSE 318
 Db 255 DTR-INSANGLEIKSTGQSLLVMANVTEEHGNTVCAANKLGVTNLSLYLRG-TGR 312
 QY 319 VSGTSTRACGVLLPLVLLHLK 343
 Db 313 VDNGSVSLAVPLMLLAASLLCLSK 337

RESULT 11

LAMP RAT STANDARD; PRT; 338 AA.
 AC Q62813;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Limbic system-associated membrane protein precursor (LSAMP).
 GN LSAMP OR LAMP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 29-49.
 RC TISSUE-Hippocampus;
 RA MEDLINE=95374785; PubMed=7646886;
 RA Pimenta A.F., Zhukareva V., Barbe M.F., Reinoso B.S., Grimley C.,
 RA Henzel W., Fischer I., Levitt P.;
 RT "The limbic system-associated membrane protein is an Ig superfamily
 RT member that mediates selective neuronal growth and axon targeting.";
 RL Neuron 15:287-297(1995).
 CC -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
 CC CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
 CC OF THE HYPOCAMPAL MOSSY FIBER PROJECTION.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: EXPRESSED MOSTLY BY NEURONS COMPRISED LIMBIC-
 CC ASSOCIATED CORTICAL AND SUBCORTICAL REGIONS THAT FUNCTION IN
 CC COGNITION, EMOTION, MEMORY, AND LEARNING.
 CC -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16, AT STAGE E20 IT IS

FT SIGNAL 1 27 BY SIMILARITY
FT CHAIN 28 322
FT PROPEP 323 345 MOLECULE IN MATURE FORM (POTENTIAL)
FT DOMAIN 329 345 REMOVED IN MATURE FORM (POTENTIAL)
FT DOMAIN 336 345 IG-LIKE C2-TYPE 1
FT DOMAIN 223 319 IG-LIKE C2-TYPE 2
FT DISULFID 57 115 POTENTIAL
FT DISULFID 157 202 POTENTIAL
FT DISULFID 244 296 POTENTIAL
FT CARBOHYD 44 44 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 70 70 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 140 140 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 285 285 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 293 293 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 306 306 N-LINKED (GLCNAC) (POTENTIAL)
FT LIPID 322 322 GPI-ANCHOR (POTENTIAL)
FT VARSPLIC 1 27 MGCGYLFKWLKLVVSLFLVPT -> MYHPAYWIVF
FT SATALLFIP (in isoform 2)
SQ SEQUENCE 345 AA; 38067 MW; A3181B0753F9658E CRC64;
/FTIG-VSP_002612

Query Match 69.7%; Score 1259; DB 1; Length 345;
Best Local Similarity 71.2%; Pred. No. 2.1e-92;

Matches 240; Conservative 34; Mismatches 59; Indels 4; Gaps 2;

QY 12 ISNAIFGLAALCF--OGVVRSGDGFPRKMDNVTVRGESATLRCTIDNRVTRVAM 68
DB 9 LPKCLVWVYSLRLLFLVPTGVPVVRSGDGFPRKMDNVTVRGESATLRCTIDNRVTRVAM 68
QY 69 LNRSTLYAGNDKCLDRVLLSNTQYSTEIONVDYDEGYTCVOTDNHPTSRV 128
DB 69 LNRSTLYAGNDKSIDRVLLVNTPTQYSTEIONVDYDEGYTCVOTDNHPTSRV 128
QY 129 HLIVQVSPKIVEISSDINSGNNISLTGATGRPEPTVTRHISPK-AGVFSDEYLE 187
DB 129 HLIVQVPPQIMISSDIIVNEISSVLLCLALGRPEPTVTRHLSYKQGGFVSEYLE 188
QY 188 IQGITEQSGDECSASNDVNAAPVVRVKNVYVPPYISEAKGTGVPVQKGTLOCESA 247
DB 189 ISDKRQSGECSALNDVNAAPVVRVKNVYVPPYISEAKGTGVPVQKGTLOCESA 248
QY 248 VPSAEQWYKDKRLECKGKGVKNRPFSLKLIFFNVSEHDYNTYCVASKNGLHTNAS 307
DB 249 VPMAEQWYKDKRLECKGKGVKNRPFSLKLIFFNVSEHDYNTYCVASKNGLHTNAS 308
QY 308 IMLEFGPQVSEVSNCTSRACGCVLLPLLVLLHLLKF 344
DB 309 ITLYGPGVADGVNSASRALCLWLSGTFFFAHFFIKF 345

RESULT 9

LAMP_CHICK STANDARD; PRT; 338 AA.
ID LAMP_CHICK STANDARD; PRT; 338 AA.
AC Q98919;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Limbic system-associated membrane protein precursor (E19S) (CHLAMP, G19-isoform)
DE Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
CX NCBI-TaxID=9031;
RN RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=97157768; PubMed=9004047;
RA Wilson D.J.A., Kim D.S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
K: "A family of glycoproteins (gp55), which inhibit neurite outgrowth,
RT are members of the Ig superfamily and are related to OBCAM,
neurotrophin, LAMP and CEPU-1."

RL J. Cell Sci. 109:3129-3138(1996).
RN SEQUENCE FROM N.A.
RP TISSUE-Brain;
RC MEDLINE=97158596; PubMed=9215692;
RA Brummendorf T., Spaltmann F., Treubert U.;
RT "Cloning and characterization of a neural cell recognition molecule on axons of the retinotectal system and spinal cord."
RL Eur. J. Neurosci. 9:1105-1116(1997).
CC -1- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CC PROBABLY SERVES AS A RECOGNITION MOLECULE FOR THE FORMATION OF.
CC LIMBIC CONNECTIONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON SUBFAMILY.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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CC EMBL: Y08171; CRA69357.1;
CC EMBL: 294720; CAB08115.1;
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003598; Ig_c2.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam: PF00047; Ig_3.
CC SMART: SM00408; IGc2; 2.
CC PROSITE: PS50935; IG-LIKE_3.
CC Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; SIGNAL; Signal;
CC CHAIN 29 338 POTENTIAL.
FT PROPEP 29 338 LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT DOMAIN 29 338 PROTEIN.
FT DOMAIN 132 214 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 219 306 IG-LIKE C2-TYPE 1.
FT DISULFID 53 111 IG-LIKE C2-TYPE 2.
FT DISULFID 153 197 POTENTIAL.
FT DISULFID 239 290 POTENTIAL.
FT CARBOHYD 40 40 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC) (POTENTIAL).
SQ SEQUENCE 338 AA; 37394 MW; 8FA4A60AD98426B4 CRC64;
Query Match 52.0%; Score 938.5; DB 1; Length 338;
Best Local Similarity 56.0%; Pred. No. 4.7e-67;
Matches 182; Conservative 56; Mismatches 82; Indels 5; Gaps 4;
QY 20 LAALCLF-OGVVRSGDGFPRKMDNVTVRGESATLRCTIDNRVTRVAMLRSTLYAG 78
DB 17 LRLCLLPTGLPVRVD--FTRGDNITVRGDTAILRDRSKRVAMLRSGIIFAG 74
QY 79 NDKWCLDRVLLSNTQYSTEIONVDYDEGYTCVOTDNHPTSRVHLIVQVSPKI 138
DB 75 EKWSLDRPRLEKRSPLYSRLQKVDYDEGYTCVOTDNHPTSRVHLIVQVSPKI 134
QY 139 VEISDSISINEGNNISLTGATGRPEPTVTRHISPKAVGFSDEYLEIQGITEQSGD 198
DB 135 SNISDSISINEGNNISLTGATGRPEPTVTRHISPKAVGFSDEYLEIQGITEQSGK 194
QY 199 YECASNDVNAAPVVRVKNVYVPPYISEAKGTGVPVQKGTLOCESAAPSABFOWYKD 258

RX MEDLINE-99251576; PubMed-2721489;
 RA Schofield P.R., McFarland K.C., Hayflick J.S., Wilcox J.N.,
 RT Cho T.M., Roy S., Lee N.M., Loh H.H., Seeburg P.H.;
 RT Molecular characterization of a new immunoglobulin superfamily
 RT protein with potential roles in opioid binding and cell contact.
 RL EMBO J. 8:489-495(1989).
 CC -!- FUNCTION: Binds opioids in the presence of acidic lipids; probably
 CC involved in cell contact.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
 CC SUBFAMILY.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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 CC
 CC EMBL; X12672; CAA31192.1;
 CC PIR; S03199;
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003598; Ig_C2.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig_3.
 CC SMART; SM00408; IgC2; 2.
 CC PROSITE; PS50835; IG-LIKE; 3.
 CC Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 KW Repeat; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 322
 FT
 FT PROPEP 323 345
 FT DOMAIN 39 126
 FT DOMAIN 136 219
 FT DOMAIN 223 310
 FT DISULFID 57 105
 FT DISULFID 157 202
 FT DISULFID 244 296
 FT CARBOHYD 44 44
 FT CARBOHYD 70 70
 FT CARBOHYD 140 140
 FT CARBOHYD 285 285
 FT CARBOHYD 293 293
 FT CARBOHYD 306 306
 FT LIPID 322 322
 FT SEQUENCE 345 AA; 37914 MW; 1266; DB 1; Length 345;
 Query Match
 Best Local Similarity 71.6%; Pred. No. 5.9e-93;
 Matches 240; Conservative 34; Mismatches 57; Indels 4; Gaps 2;
 QY 14 WAIFGTGALALCLF---QGVPRSGDATFPKAMDNVTVROGESATLRCITDNRVTRVAVLN 70
 DB 11 WKLVVYSLRLFLVPTGVPVRSRGDATFPKAMDNVTVROGESATLRCITDNRVTRVAVLN 70
 QY 71 RSTLYAGNCKWCLDRVLLSNLTQYSIEIQNVYDVGPTCSVQTDNHPKTSRVHL 130
 DB 71 RSTLYAGNCKWCLDRVLLSNLTQYSIEIQNVYDVGPTCSVQTDNHPKTSRVHL 130
 QY 131 IVQSPKIVEISSDISISNEGNNISLFCIATGRPEPTVTRHISPK-AVGFSVEDEYLEIQ 189
 DB 131 IVQSPKIVEISSDISISNEGNNISLFCIATGRPEPTVTRHISPK-AVGFSVEDEYLEIQ 189
 QY 190 GTTRQSGDGYECSASNDVAAPVVRVKKVTVNPPYVISEAKGTGVPVGQGTQCEASAVP 249
 DB 191 DIKRDQSGEYCSALNDVAAPVVRVKKVTVNPPYVISEAKGTGVPVGQGTQCEASAVP 250
 QY 250 SAFQWYKDKRLTEGKGVKVENRFLSKLTFNVSEHDYGNVTCVASKLHTNASIM 309
 DB 250 SAFQWYKDKRLTEGKGVKVENRFLSKLTFNVSEHDYGNVTCVASKLHTNASIM 309

DB 251 MAEFQWFKEDTRLATGDMRIENKGHISTLTFNFVSEKDYGNVTCVATNKLGTNASIT 310
 QY 310 LFGPGAVSEVSNSTSRACGVWLLPLVLVHLHLKF 344
 DB 311 LYGPAGVTDGVNSASRALACLWLSGLTFAFFIKF 345
 RESULT 8
 OPCML RAT
 ID OPCML RAT STANDARD; PRT: 345 AA.
 AC P32736; P32735; Q01653; Q01654;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Opioid binding protein/cell adhesion molecule precursor (OBCAM)
 GN Opioid-binding cell adhesion molecule (OPCML).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE-92347701; PubMed-1339369;
 RT Lippman D.A., Lee N.M., Loh H.H.;
 RT "Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
 RT rat brain cDNA library."
 RL Gene 117:249-254(1992).
 RN [2]
 RN SEQUENCE OF 195-214. AND GPI-ANCHOR.
 RA MEDLINE-95198094; PubMed-7831157;
 RA Struyk A.F., Canoll P.D., Wolfgang M.J., D'Eustachio P.,
 RA Salzer J.L.;
 RT "Cloning of neurotrophin defines a new subfamily of differentially
 RT expressed neural cell adhesion molecules."
 RL J. Neurosci. 15:2141-2156(1995).
 CC -!- FUNCTION: Binds opioids in the presence of acidic lipids; probably
 CC involved in cell contact.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-2;
 CC Comment-Additional isoforms seem to exist;
 CC Name-1;
 CC Name-2;
 CC IsoId=P32736-1; Sequence-Displayed;
 CC Note-No experimental confirmation available;
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
 CC SUBFAMILY.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M88710; AAA40859.1;
 CC EMBL; M88711; AAA40860.1;
 CC PIR; JG1238; JG1238.
 CC PIR; JG1239; JG1239.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003598; Ig_C2.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig_3.
 CC SMART; SM00408; IgC2; 2.
 CC PROSITE; PS50835; IG-LIKE; 3.
 CC Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 KW Repeat; Signal; Alternative splicing.

QY 8 MNSTSWAIFTGLAALCLFQGVVPSRGDAATFPKAMDNVTVRQGESATLCTIDNRVTRVA 67
DB 1 MYHPACWTFVATTALLFPVPSRGDAATFPKAMDNVTVRQGESATLCTIDNRVTRVA 60
QY 68 WLNSTILYAGNDKWCIDPRVLLSNTQYSIIEQNVVDYDEGPTCSVQTDNHPKTSR 127
DB 61 WLNSTILYAGNDKWCIDPRVLLSNTQYSIIEQNVVDYDEGPTCSVQTDNHPKTSR 120
QY 128 VHLIVQVSPKVEISSDISINEGNNISLCTATGRPEPTVTRHISPKAVGFVSEDEYLE 187
DB 121 VHLIVQVSPKVEISSDISINEGNNISLCTATGRPEPTVTRHISPKAVGFVSEDEYLE 180
QY 188 IOGITREQSGDYECASNDVAAPVRRVKKVTNNPPYVISEAKGTGVPVQKGTLCQCEASA 247
DB 181 ITGITREQSGDYECASNDVAAPVRRVKKVTNNPPYVISEAKGTGVPVQKGTLCQCEASA 240
QY 248 VPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 307
DB 241 VPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 300
QY 308 IMLEFGGAVSEVSGTSSRRAG--CVWLLPPLVLLHLLK 344
DB 301 ILYGFGAVHDSGNAASRAAGLCW--ATLARELLIDF 337

RESULT 6
OPCM_HUMAN STANDARD; PRT; 345 AA.
AC Q14982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Opioid binding protein/cell adhesion molecule precursor (OBSCAM)
DE (Opioid-binding cell adhesion molecule) (OPCML)
GN OPCML OR OBSCAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Occipital cortex;
RX MEDLINE=95237612; PubMed=7721093;
RA Shark K.B., Lee N.M.;
RT "Cloning, sequencing and localization to chromosome 11 of a cDNA
RT encoding a human opioid-binding cell adhesion molecule (OBSCAM).";
RL Gene 155:213-217(1995).
CC -!- FUNCTION: Binds opioids in the presence of acidic lipids; probably
CC involved in cell contact.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUPERFAMILY.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L34774; AAA36387.1;
CC PIR; J4025; JC4025.
CC Genbank; HGNC:8143; OPCML.
CC MIM; 600632;
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0004985; F: opioid receptor activity; TAS.
CC GO; GO:0007155; P: cell adhesion; TAS.
CC GO; GO:0008038; P: neuronal cell recognition; TAS.
CC InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 12.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal.
FT SIGNAL 1 27
FT CHAIN 28 322
FT BY SIMILARITY.
FT OPIOID BINDING PROTEIN/CELL ADHESION
FT MOLECULE.
FT REMOVED IN MATURE FORM (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT IG-LIKE C2-TYPE 3.
FT POTENTIAL.
FT POTENTIAL.
FT POTENTIAL.
FT POTENTIAL.
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT GPI-ANCHOR (POTENTIAL).
FT SEQUENCE 345 AA; 38007 MW; E7ADI7BEAIAA3FF4_CRC64;
Query Match 70.2%; Score 1268; DB 1; Length 345;
Best Local Similarity 71.2%; Pred. No. 4.1e-93;
Matches 240; Conservative 37; Mismatches 56; Indels 4; Gaps 2;
QY 12 ISWAIFTGLAALCLF---QGVVPSRGDAATFPKAMDNVTVRQGESATLCTIDNRVTRVA 68
DB 9 LPWCLVVSRLFLVPTGVPVPSRGDAATFPKAMDNVTVRQGESATLCTIDNRVTRVA 68
QY 69 LNRSTILYAGNDKWCIDPRVLLSNTQYSIIEQNVVDYDEGPTCSVQTDNHPKTSR 128
DB 69 LNRSTILYAGNDKWCIDPRVLLSNTQYSIIEQNVVDYDEGPTCSVQTDNHPKTSR 128
QY 129 HLIQVQSPKVEISSDISINEGNNISLCTATGRPEPTVTRHISPKAVGFVSEDEYLE 187
DB 129 HLIQVQSPKVEISSDISINEGNNISLCTATGRPEPTVTRHISPKAVGFVSEDEYLE 188
QY 188 IOGITREQSGDYECASNDVAAPVRRVKKVTNNPPYVISEAKGTGVPVQKGTLCQCEASA 247
DB 189 ISDIKRDQSGDYECASNDVAAPVRRVKKVTNNPPYVISEAKGTGVPVQKGTLCQCEASA 248
QY 248 VPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 307
DB 249 VPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 308
QY 308 IMLEFGGAVSEVSGTSSRRAG--CVWLLPPLVLLHLLK 344
DB 309 ILYGFGAVHDSGNAASRAAGLCW--ATLARELLIDF 345

RESULT 7
OPCM_BOVIN STANDARD; PRT; 345 AA.
AC P11634;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Opioid binding protein/cell adhesion molecule precursor (OBSCAM)
DE (Opioid-binding cell adhesion molecule) (OPCML).
GN OPCML OR OBSCAM OR OCAM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RC TISSUE=Brain;

ACTIVITY: Contains 3 immunoglobulin-like C2-type domains.

EMBL: Z72497; CAA96578.1; -
InterPro: IPR007110; Ig-like.

SMART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_LIKE; 3.

EXPERIMENTAL	THEORY	PERCENTAGE
29	330	CEPU-1 PROTEIN.
331	353	REMOVED IN MATURE FORM (POTENTIAL).

DISULFID	55	POTENTIAL.
DOMAIN	220	IG-LIKE C2-TYPE 3.
	314	
DISULFID	55	POTENTIAL.
DISULFID	155	POTENTIAL.
	199	

Compound	68	150	282	68	150	282
CARBOHYD	68	150	282	N-LINKED	(GLCNAC.	(POTENTIAL).
CARBOHYD	68	150	282	N-LINKED	(GLCNAC.	(POTENTIAL).
CARBOHYD	68	150	282	N-LINKED	(GLCNAC.	(POTENTIAL).
CARBOHYD	68	150	282	N-LINKED	(GLCNAC.	(POTENTIAL).

LIPID	330	330	GPI-ANCHOR (POTENTIAL)
VARSPPLIC	310	320	Missing (in isoform 2)

ry Match	81.8%;	Score 1477.5;	DB 1;	Length 353;
t Local Similarity	78.6%;	Pred. No. 1.1e-109;		

3 QAKMQHPVSWVIFAGMAALLLFGQVPRSGDATFPKAMDNVTVRQGESATLRCSDNRVT 62

63. RYAWLNRSSILYAGNDKWCLDPVLLANTKTQYSIQIHVDVYDEGPYTCVQTDNHPK 122

123 TSRVHLIVQSPKINETSSDISINEGGNSVLTCTIATGRPDPTITWRHISPRKAVGFISEDE 182

245 ASAPVSAEFQWYKDDKRLLIEGKKGKVKVENPPFLSKLIFFNVSEHDYGNVTCVASNKLGHT 304

305 NASIMLF-----GPCAYSEVSNCTSRAGCVWLLPLLVLHLLKF 344
|||||: : ||||| : : ||||| : : ||||| : : ||||| : :

CC
DR

EMBL; Y08170; CAB41420.1; -

DR Pfam; PF00047; 1g.3.
DR SMART; SM00408; IGC2; 2.

FT	Signal	20	BY SIMILARITY.
FT	Repeat; signal	1	
FT	SIGNAL	21	NEURITE INHIBITOR GP55-A (POTENTIAL).

FT	DOMAIN	IG-LIKE C2-TYPE 2.	IG-LIKE C2-TYPE 3.	DOMAINS
FT	129	211		
FT	215	302		
FT	50	109		

FT	CARBOHYD	133	N-LINKED (GLCNAC: .)	(POTENTIAL)
FT	CARBOHYD	277	N-LINKED (GLCNAC: .)	(POTENTIAL)

Query Match 72.3% Score 1305 DB 1: Length 337:
SEQUENCE 337 AA: 3066 MW: 84671.1/331630031E CRC04;


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FT CARBOHYD 305 305 N-LINKED (GLCNAC... ) (POTENTIAL);
FT CARBOHYD 321 321 N-LINKED (GLCNAC... ) (POTENTIAL);
FT LIPID 321 321 GPI-ANCHOR (POTENTIAL);
SQ SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;

Query Match
Best Local Similarity 92.2%; Score 1665.5; DB 1; Length 344;
Matches 320; Conservative 3; Mismatches 10; Indels 3; Gaps 1;

QY 12 ISWAFITGLAALCLF---OGVPSRSGDATFPKAMDNVTVRQGESATLCTIDNRTVAV 68
DB 9 LPKCLVSVLSRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLCTIDNRTVAV 68
QY 69 LNRSTILYAGNDKWCIDPRVLLSNTQYISIEIQNVYDDEGPTCSVQDNHPTKTSRV 128
DB 69 LNRSTILYAGNDKWCIDPRVLLSNTQYISIEIQNVYDDEGPTCSVQDNHPTKTSRV 128
QY 129 HLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLEI 188
DB 129 HLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLEI 188
QY 189 OGITREQSGDYECASNDVAAPVVRVKVTNVPYISSEAKGTGVPVQKGTLOCESAV 248
DB 189 OGITREQSGDYECASNDVAAPVVRVKVTNVPYISSEAKGTGVPVQKGTLOCESAV 248
QY 249 PSAEFQWKDKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNASI 308
DB 249 PSAEFQWKDKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNASI 308
QY 309 MLFGPGAVSEVSGTSRRAGCVLLPLVLVLLHLKLF 344
DB 309 MLFGPGAVSEVSGTSRRAGCVLLPLVLVLLHLKLF 344

RESULT 2
NTRI_MOUSE STANDARD; PRT: 344 AA.
ID NTRI_MOUSE STANDARD; PRT: 344 AA.
AC 099P70;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=; TISSUE=Brain;
RA Kim.T.H., Choi S.C., Kim J., Jeon J.W., Kim K.D., Lee S.H.;
RT "Cloning and expression of mouse neurotrophin gene in the developing
RL nervous system."
RN Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Eye;
RX MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,
RA Richards S., Worley D.M., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettman M., Vadan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full
RL human and mouse cDNA sequences."
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anch
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaborati
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announc/
CC or send an email to license@isb-sib.ch).
CC EMBL; AF282980; RAK00276.1;
CC EMBL; BC023307; RAH23307.1;
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR003598; IG_C2.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; IG; 3.
CC SMART; SM00409; IG; 3.
CC SMART; SM00408; IGC2; 3.
CC PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 321. NEUROTRPHIN
FT PROPEP 322 344. REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 126. IG-LIKE C2-TYPE 1.
FT DOMAIN 136 218. IG-LIKE C2-TYPE 2.
FT DOMAIN 222 309. IG-LIKE C2-TYPE 3.
FT DISULFID 157 201. POTENTIAL.
FT DISULFID 157 201. POTENTIAL.
FT CARBOHYD 243 295. POTENTIAL.
FT CARBOHYD 44 44. N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 152 152. N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 284 284. N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 292 292. N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 305 305. N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 321 321. N-LINKED (GLCNAC... ) (POTENTIAL).
FT LIPID 321 321. GPI-ANCHOR (POTENTIAL).
FT CONFLICT 75 75. L -> P (IN REF. 1).
FT CONFLICT 92 92. S -> G (IN REF. 1).
FT CONFLICT 119 119. T -> I (IN REF. 1).
FT CONFLICT 187 187. E -> Q (IN REF. 1).
FT CONFLICT 213 213. R -> P (IN REF. 1).
FT CONFLICT 225 225. I -> F (IN REF. 1).
SQ SEQUENCE 344 AA; 37984 MW; C885BBA52C148554 CRC64;

Query Match
Best Local Similarity 91.2%; Score 1647.5; DB 1; Length 344;
Matches 314; Conservative 8; Mismatches 11; Indels 3; Gaps 1;

QY 12 ISWAFITGLAALCLF---OGVPSRSGDATFPKAMDNVTVRQGESATLCTIDNRTVAV 68
DB 9 LPKCLVSVLSRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLCTIDNRTVAV 68
QY 69 LNRSTILYAGNDKWCIDPRVLLSNTQYISIEIQNVYDDEGPTCSVQDNHPTKTSRV 128
DB 69 LNRSTILYAGNDKWCIDPRVLLSNTQYISIEIQNVYDDEGPTCSVQDNHPTKTSRV 128
QY 129 HLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLEI 188
DB 129 HLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLEI 188
QY 189 OGITREQSGDYECASNDVAAPVVRVKVTNVPYISSEAKGTGVPVQKGTLOCESAV 248
DB 189 OGITREQSGDYECASNDVAAPVVRVKVTNVPYISSEAKGTGVPVQKGTLOCESAV 248

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 02:51:48 ; Search time 34 Seconds
(without alignments)
475.800 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 1806

Sequence: 1 MKTIQPKMHSNWSIAFTGL.....RRAGCVWLLPLVLHLLKLF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs., 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1655.5	92.2	344	1	NTRI_HUMAN
2	1647.5	91.2	344	1	NTRI_MOUSE
3	1639.5	90.8	344	1	NTRI_RAT
4	1477.5	81.8	353	1	CEPU_CHICK
5	1305	72.3	337	1	G55A_CHICK
6	1268	70.2	345	1	OFCM_HUMAN
7	1266	70.1	345	1	OFCM_BOVIN
8	1259	69.7	345	1	OFCM_RAT
9	938.5	52.0	338	1	LAMP_CHICK
10	931.5	51.6	338	1	LAMP_HUMAN
11	926.5	51.3	338	1	LAMP_RAT
12	815	45.1	348	1	KILO_RAT
13	297.5	16.5	333	1	AMAL_DROME
14	283.5	15.7	725	1	NCA2_MOUSE
15	283.5	15.7	1115	1	NCA1_MOUSE
16	279.5	15.5	1091	1	NCA1_CHICK
17	277.5	15.4	858	1	NCA1_RAT
18	277.5	15.4	1088	1	NCA1_XENLA
19	276	15.3	761	1	NCA2_HUMAN
20	276	15.3	848	1	NCA1_HUMAN
21	275.5	15.3	853	1	NCA1_BOVIN
22	270.5	15.0	1092	1	NCA2_XENLA
23	261.2	14.5	1010	1	CONT_CHICK
24	255	14.1	359	1	LACH_DROME
25	251.5	13.9	837	1	NCA2_MOUSE
26	250	13.8	349	1	LACH_SCHAM
27	249.5	13.8	1040	1	AXO1_HUMAN
28	246.5	13.6	1018	1	CONT_HUMAN
29	243.5	13.5	1021	1	CONT_RAT
30	243.5	13.5	1036	1	AXO1_CHICK
31	241.5	13.4	837	1	NCA2_HUMAN
32	241.5	13.4	1020	1	CONT_MOUSE
33	240	13.3	3707	1	PGBM_MOUSE

34	234.5	13.0	1040	1	AXO1_RAT
35	229	12.7	4391	1	PGBM_HUMAN
36	227.5	12.6	1051	1	PTK7_CHICK
37	226	12.5	6632	1	UN69_CAEEL
38	221.5	12.3	862	1	CD22_MOUSE
39	221	12.2	2012	1	DSCA_HUMAN
40	220.5	12.2	896	1	FAS2_SCHAM
41	215.5	11.9	1302	1	NRC_DROME
42	211.5	11.7	873	1	FAS2_DROME
43	211.5	11.7	1070	1	PTK7_HUMAN
44	211.5	11.7	1461	1	NEO1_HUMAN
45	210	11.6	1914	1	KMLS_HUMAN

ALIGNMENTS

RESULT 1
NTRI_HUMAN
ID NTRI_HUMAN STANDARD; PRT; 344 AA.
AC Q9P121;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor (hnt).
GN NT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Jin J., Pan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrophin full length cDNA."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Neural cell adhesion molecule.
CC -1- CELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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EMBL; AF126426; AAF37591.1;
GO; GO:0008038; P:neuronal cell recognition; TAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-C2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00408; IgC2; 2.
PROSITE; PS00835; IG_LIKE; 3.
Immunoglobulin domain; Cell adhesion; G
Repeat; Signal.
FT SIGNAL; 1
FT CHAIN; 31
FT POTENTIAL.
FT NEUTROTRIMI
FT REMOVED IN
FT IG-LIKE C2
FT 324
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FT 17
FT 16
FT 15
FT 14
FT 13
FT 12
FT 11
FT 10
FT 9
FT 8
FT 7
FT 6
FT 5
FT 4
FT 3
FT 2
FT 1

Db 301 LGHTNASIMLFGPAGVSEVSNGTSRAGCVLLPLVLLHLLKF 344

RESULT 15
AAM40499

ID AAM40499 standard; Protein; 355 AA.
AC AAM40499;
XX
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 5430.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN W0200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR -09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang J, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB: AAI59655.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as: central nervous system injuries -
XX
PS Example 2; SEQ ID NO 5430; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 355 AA:

Query Match 100.0%; Score 1806; DB 22; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.2e-149;

	Matches	344;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	MKTIOPKMNSISWALFTGLAALCLFQGVVPRSGDATPPKAMDNVTVRQGESATLRCTID	60							
Db	12	MKTIOPKMNSISWALFTGLAALCLFQGVVPRSGDATPPKAMDNVTVRQGESATLRCTID	71							
QY	61	NRVTRVAMLRSTILYAGNDKWCCLDPRVLLSNTQFQYSIEIQNVVDYDEGPTCVSQVD	120							
Db	72	NRVTRVAMLRSTILYAGNDKWCCLDPRVLLSNTQFQYSIEIQNVVDYDEGPTCVSQVD	131							
QY	121	NHPKTSRVHLIVOVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHISPKAVGFV	180							
Db	132	NHPKTSRVHLIVOVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHISPKAVGFV	191							
QY	181	SEDEYLEIOGITREQSGDYECSSASNDVAAPVVRVKVTVPYPPYISEAKGTGVPVGQKGT	240							
Db	192	SEDEYLEIOGITREQSGDYECSSASNDVAAPVVRVKVTVPYPPYISEAKGTGVPVGQKGT	251							
QY	241	LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK	300							
Db	252	LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK	311							
QY	301	LGHTNASIMLFGPAGVSEVSNGTSRAGCVLLPLVLLHLLKF	344							
Db	312	LGHTNASIMLFGPAGVSEVSNGTSRAGCVLLPLVLLHLLKF	355							

Search completed: September 11, 2003, 03:02:43
Job time : 74 secs

PR 16-DEC-1999; 99WO-US30095
PR 30-DEC-1999; 99WO-US31243
PR 30-DEC-1999; 99WO-US31274
PR 03-JAN-2000; 2000WO-US300219
PR 08-JAN-2000; 2000WO-US300377
PR 16-JAN-2000; 2000WO-US300576
PR 18-FEB-2000; 2000WO-US303565
PR 24-FEB-2000; 2000WO-US304341
PR 02-MAR-2000; 2000WO-US305004
PR 10-MAR-2000; 2000WO-US305841
PR 21-MAR-2000; 2000WO-US306319
PR 30-MAR-2000; 2000WO-US307532
PR 17-MAY-2000; 2000WO-US308439
PR 22-MAY-2000; 2000WO-US313705
PR 30-MAY-2000; 2000WO-US14042
PR 02-JUN-2000; 2000WO-US14941
PR 28-JUL-2000; 2000WO-US20710
PR 24-AUG-2000; 2000WO-US23328
PR 01-DEC-2000; 2000WO-US32678
PR 20-DEC-2000; 2000WO-US34956
PR 28-FEB-2001; 2001WO-US06520
PR 22-MAR-2001; 2001WO-US09552
PR 25-MAY-2001; 2001WO-US17092
PR 01-JUN-2001; 2001WO-US17800
PR 20-JUN-2001; 2001WO-US19692
PR 29-JUN-2001; 2001WO-US21066
PR 09-JUL-2001; 2001WO-US21735
PR 17-OCT-1997; 97US-062250P
PR 03-NOV-1997; 97US-064249P
PR 13-NOV-1997; 97US-065311P
PR 21-NOV-1997; 97US-066364P
PR 10-MAR-1998; 98US-077450P
PR 11-MAR-1998; 98US-077632P
PR 11-MAR-1998; 98US-077641P
PR 12-MAR-1998; 98US-077649P
PR 12-MAR-1998; 98US-077791P
PR 20-MAR-1998; 98US-078004P
PR 20-MAR-1998; 98US-078866P
PR 20-MAR-1998; 98US-078910P
PR 20-MAR-1998; 98US-078939P
PR 20-MAR-1998; 98US-078939P
PR 26-MAR-1998; 98US-079294P
PR 27-MAR-1998; 98US-079636P
PR 27-MAR-1998; 98US-079664P
PR 27-MAR-1998; 98US-079689P
PR 27-MAR-1998; 98US-079728P
PR 30-MAR-1998; 98US-079786P
PR 30-MAR-1998; 98US-079920P
PR 26-MAY-1981; 81US-0267213
PR 17-MAR-1998; 98US-0040220
PR 26-JUN-1998; 98US-0105413
PR 07-OCT-1998; 98US-0168978
PR 02-NOV-1998; 98US-0184216
PR 06-NOV-1998; 98US-0187368
PR 07-DEC-1998; 98US-0202054
PR 22-DEC-1998; 98US-0218517
PR 05-MAR-1999; 99US-0254465
PR 10-MAR-1999; 99US-0265686
PR 12-APR-1999; 99US-0284291
PR 14-MAY-1999; 99US-0311832
PR 25-AUG-1999; 99US-0380137
PR 25-AUG-1999; 99US-0380138
PR 03-NOV-2000; 2000US-0709238
PR 27-NOV-2000; 2000US-0723749
PR 20-DEC-2000; 2000US-0747259
PR 22-MAR-2001; 2001US-0816744
PR 22-MAR-2001; 2001US-0816920
PR 10-MAY-2001; 2001US-0854208
PR 10-MAY-2001; 2001US-0854280

PR 01-JUN-2001; 2001US-0872035
PR 05-JUN-2001; 2001US-0874503
PR 14-JUN-2001; 2001US-0882636
PR 19-JUN-2001; 2001US-0886342
PR 30-JUL-2001; 2001US-0918585
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Flivvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2003-288163/28.
DR N-PSDB; ABX92696.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies
XX
PS Claim 12; Fig 222; 459pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC AB061071-AB061164 represent the human PRO polypeptides of the
CC invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdEntry.html.
XX
XX Sequence 344 AA;
SQ
Query Match 100.0%; Score 1806; DB 24; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTIQPKMHSISWAIFTGLAALCLFGQVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
Db 1 MKTIQPKMHSISWAIFTGLAALCLFGQVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
QY 61 NRVTRVAVLNRSTILYAGNDKWCIDPRVLLSNTQTSIQRNVYDYGPTCSVQTD 120
Db 61 NRVTRVAVLNRSTILYAGNDKWCIDPRVLLSNTQTSIQRNVYDYGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCATGRPTTWHHSIPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCATGRPTTWHHSIPKAVGFV 180
QY 181 SEDEYLEIQCITREOSGDYECASNDVAPVRRVKVTNTPPIISAKGTGVPVQKGT 240
Db 181 SEDEYLEIQCITREOSGDYECASNDVAPVRRVKVTNTPPIISAKGTGVPVQKGT 240
QY 241 LQCEASAVPSAEFQWKDKRLIEGKKGKGVKNRPFLLSKLIFFNVSEHDYNTCVASNK 300
Db 241 LQCEASAVPSAEFQWKDKRLIEGKKGKGVKNRPFLLSKLIFFNVSEHDYNTCVASNK 300
QY 301 LGHTNASIMLFGFGAVSEVSNGTSSRAGCVMLLPLVLLHLLK 344

CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (ii) Is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (i) Or Ab is useful for the preparation of medicament or
 CC treating conditions which are responsive to the PRO polypeptide or
 CC anti-PRO antibody e.g. a tumour. (ii) Is useful for treating obesity,
 CC diabetes or hypo- or hyper-insulinemia, and cardiac insufficiency
 CC disorders, for inhibiting tumour growth, enhances vascular permeability
 CC and immune response, for inducing regeneration of auditory hair cells and
 CC for treating hearing loss in mammals, and for treating bone and/or
 CC cartilage disorders such as sports injuries and arthritis. This is the
 CC amino acid sequence of a novel human secreted and transmembrane
 CC polypeptide associated oligonucleotide.

XX Sequence 344 AA;

Query Match 100.0%; Score 1806; DB 24; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKHNSISWAIETGLAALCLFQGVVRSNGDAPPRAMDNVTVROGESATLRCTID 60
 DB 1 MKTIQPKHNSISWAIETGLAALCLFQGVVRSNGDAPPRAMDNVTVROGESATLRCTID 60

QY 61 NRVTRVAMLNSTLYAGNDKWCIDPRVLLSNTOQTSIEIONVDYDEGYTCVSQTD 120
 DB 61 NRVTRVAMLNSTLYAGNDKWCIDPRVLLSNTOQTSIEIONVDYDEGYTCVSQTD 120

QY 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHISPRKAVGV 180
 DB 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHISPRKAVGV 180

QY 181 SEDEYLEIQTIGTREQSGDYECSSASNDVAAAPVVRVVKVTVNPPYIIEAKGTGVPVQKGT 240
 DB 181 SEDEYLEIQTIGTREQSGDYECSSASNDVAAAPVVRVVKVTVNPPYIIEAKGTGVPVQKGT 240

QY 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
 DB 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300

QY 301 LGHTNASIMLFGPGAVSEVSNGTSSRAGCVLLPLVLLHLLKF 344
 DB 301 LGHTNASIMLFGPGAVSEVSNGTSSRAGCVLLPLVLLHLLKF 344

RESULT 13

ABU5983B
 ID ABU5983B standard; Protein; 344 AA.

XX ABU5983B;

XX 13-MAY-2003 (first entry)

DE Novel secreted and transmembrane protein PR0337.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 OS Homo sapiens.

PN US2003017563-A1
 XX 23-JAN-2003.
 XX 07-MAY-2002; 2002US-0140808.
 XX 31-MAR-1997; 97WO-US05230.
 XX 12-JUN-1998; 98WO-US12456.
 XX 14-JUN-1998; 98WO-US14552.
 XX 28-AUG-1998; 98WO-US17888.
 XX 10-SEP-1998; 98WO-US18824.
 XX 14-SEP-1998; 98WO-US19093.
 XX 14-SEP-1998; 98WO-US19094.
 XX 14-SEP-1998; 98WO-US19177.
 XX 16-SEP-1998; 98WO-US19330.
 XX 17-SEP-1998; 98WO-US19437.
 XX 07-OCT-1998; 98WO-US21141.
 XX 29-OCT-1998; 98WO-US22991.
 XX 29-OCT-1998; 98WO-US22992.
 XX 01-DEC-1998; 98WO-US24855.
 XX 05-JAN-1999; 98WO-US25108.
 XX 08-MAR-1999; 98WO-US00106.
 XX 10-MAR-1999; 98WO-US05028.
 XX 20-APR-1999; 98WO-US05190.
 XX 14-MAY-1999; 98WO-US08615.
 XX 02-JUN-1999; 98WO-US10733.
 XX 08-SEP-1999; 98WO-US12252.
 XX 13-SEP-1999; 98WO-US20111.
 XX 13-SEP-1999; 98WO-US20594.
 XX 15-SEP-1999; 98WO-US20944.
 XX 15-SEP-1999; 98WO-US21090.
 XX 05-OCT-1999; 98WO-US21547.
 XX 29-NOV-1999; 98WO-US23089.
 XX 30-NOV-1999; 98WO-US28214.
 XX 30-NOV-1999; 98WO-US28313.
 XX 01-DEC-1999; 98WO-US28409.
 XX 01-DEC-1999; 98WO-US28301.
 XX 02-DEC-1999; 98WO-US28531.
 XX 02-DEC-1999; 98WO-US28564.
 XX 02-DEC-1999; 98WO-US28565.
 XX 16-DEC-1999; 98WO-US30095.
 XX 20-DEC-1999; 98WO-US30911.
 XX 20-DEC-1999; 98WO-US30999.
 XX 22-DEC-1999; 98WO-US31243.
 XX 30-DEC-1999; 98WO-US31274.
 XX 05-JAN-2000; 2000WO-US00219.
 XX 06-JAN-2000; 2000WO-US00277.
 XX 11-FEB-2000; 2000WO-US00376.
 XX 18-FEB-2000; 2000WO-US03565.
 XX 18-FEB-2000; 2000WO-US04341.
 XX 22-FEB-2000; 2000WO-US04342.
 XX 24-FEB-2000; 2000WO-US04414.
 XX 24-FEB-2000; 2000WO-US04914.
 XX 01-MAR-2000; 2000WO-US05004.
 XX 02-MAR-2000; 2000WO-US05501.
 XX 02-MAR-2000; 2000WO-US05746.
 XX 10-MAR-2000; 2000WO-US05841.
 XX 15-MAR-2000; 2000WO-US06319.
 XX 20-MAR-2000; 2000WO-US06884.
 XX 21-MAR-2000; 2000WO-US07377.
 XX 30-MAR-2000; 2000WO-US07532.
 XX 17-MAY-2000; 2000WO-US08439.
 XX 22-MAY-2000; 2000WO-US13705.
 XX 30-MAY-2000; 2000WO-US14042.
 XX 02-JUN-2000; 2000WO-US14941.
 XX 28-JUL-2000; 2000WO-US15264.
 XX 11-AUG-2000; 2000WO-US20710.
 XX 23-AUG-2000; 2000WO-US22031.
 XX 24-AUG-2000; 2000WO-US23522.
 XX 08-NOV-2000; 2000WO-US23328.
 XX 08-NOV-2000; 2000WO-US30952.

DE Novel human secreted and transmembrane protein PRO337.
 XX Secreted and transmembrane polypeptide: PRO polypeptide: PRO533;
 KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO507; PRO6003;
 KW PRO6004; PRO456; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tumour; obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
 XX Homo sapiens.
 XX US2003032062-A1.
 PN 13-FEB-2003.
 XX 01-FEB-2002; 2002US-0066273;
 XX 14-JUL-1998; 98WO-US14552.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 20-NOV-1998; 98WO-US24855.
 PR 25-NOV-1998; 98WO-US25190.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-MAR-1999; 98WO-US05028.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20594.
 PR 15-SEP-1999; 98WO-US21090.
 PR 15-SEP-1999; 98WO-US21547.
 PR 30-NOV-1999; 98WO-US28313.
 PR 01-DEC-1999; 98WO-US28301.
 PR 02-DEC-1999; 98WO-US28365.
 PR 09-DEC-1999; 98WO-US30399.
 PR 18-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 01-MAR-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US05601.
 PR 09-MAR-2000; 2000WO-US05841.
 PR 20-MAR-2000; 2000WO-US06471.
 PR 30-MAR-2000; 2000WO-US07377.
 PR 15-MAY-2000; 2000WO-US08439.
 PR 22-MAY-2000; 2000WO-US13358.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 30-MAY-2000; 2000WO-US14042.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23528.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 26-AUG-1997; 97US-056974P.
 PR 17-SEP-1997; 97US-058115P.
 PR 18-SEP-1997; 97US-058263P.
 PR 19-SEP-1997; 97US-059588P.
 PR 17-OCT-1997; 97US-062283P.
 PR 24-OCT-1997; 97US-062816P.
 PR 24-OCT-1997; 97US-063082P.
 PR 27-OCT-1997; 97US-063329P.
 PR 29-OCT-1997; 97US-063733P.
 PR 21-NOV-1997; 97US-066364P.
 PR 25-NOV-1997; 97US-066840P.
 PR 16-DEC-1997; 97US-069694P.
 PR 09-FEB-1998; 98US-074086P.
 PR 09-FEB-1998; 98US-074092P.
 PR 23-MAR-1998; 98US-079294P.
 PR 08-APR-1998; 98US-081049P.
 PR 10-AUG-1998; 98US-095958P.
 PR 18-AUG-1998; 98US-097000P.
 PR 09-SEP-1998; 98US-099601P.
 PR 10-SEP-1998; 98US-099803P.
 PR 10-SEP-1998; 98US-099811P.
 PR 10-SEP-1998; 98US-099812P.
 PR 17-SEP-1998; 98US-100858P.
 PR 24-SEP-1998; 98US-101922P.
 PR 28-OCT-1998; 98US-106032P.
 PR 20-NOV-1998; 98US-109304P.
 PR 23-MAR-1999; 99US-125778P.
 PR 15-JUN-1999; 99US-139695P.
 PR 20-JUL-1999; 99US-145070P.
 PR 17-AUG-1999; 99US-145698P.
 PR 07-DEC-1999; 99US-149396P.
 PR 15-NOV-2001; 2001US-0002796.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier WA, Pan J,
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
 PI Wood WL, Zhang Z,
 XX WPI: 2003-341963/32.
 DR N-PSDB; ACA04516.
 XX New secreted and transmembrane polypeptide for modulating biological
 PI activity of a cell expressing the polypeptide, identifying agonists or
 PT antagonists of the polypeptide, and as molecular weight markers
 XX Claim 12; Fig 52; 254pp; English.
 PS The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (ii) is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (i) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or
 CC anti-PRO antibody e.g. a tumour. (i) is useful for treating obesity,
 CC diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
 CC disorders for inhibiting tumour growth, enhances vascular permeability
 CC and immune response, for inducing regeneration of auditory hair cells and
 CC for treating hearing loss in mammals, and for treating bone and/or
 CC cartilage disorders such as sports injuries and arthritis. This is the
 CC amino acid sequence of a novel human secreted and transmembrane
 CC polypeptide.
 XX Sequence 344 AA;
 SQ
 Query Match 100.0%; Score 1806; DB 24; Length 344;
 Best Local Similarity. 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTIQPKMHNISWAIFTGLAALCLFQGVPRSGDATEPKAMDNTVROGESATLRCITD 60
 DB 1 MKTIQPKMHNISWAIFTGLAALCLFQGVPRSGDATEPKAMDNTVROGESATLRCITD 60

PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 21-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US07532.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30973.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06320.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0886362.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0909827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931826.
 PR 19-DEC-2001; 2001US-0028072.
 PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-331925/31.
 DR N-PSDB; ACA04211.

XX New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer

XX PS
 XX PS
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.
 XX SQ Sequence 344 AA;

Query Match 100.0%; Score 1806; DB 24; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKTIQPKHNSISWAFITGLAALCLFQGVPRVSGDATFPKMDNVTVRQGESATLRCTID 60
 DB 1 MKTIQPKHNSISWAFITGLAALCLFQGVPRVSGDATFPKMDNVTVRQGESATLRCTID 60
 OY 61 NRVTRVWLNRSTLLIAGNDKNCLOPRVLLSNTQYSTEIQNVVDVDEGPTCSYQTD 120
 DB 61 NRVTRVWLNRSTLLIAGNDKNCLOPRVLLSNTQYSTEIQNVVDVDEGPTCSYQTD 120
 OY 121 NHPKTSRVLLIVQVSPKIVEISDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 DB 121 NHPKTSRVLLIVQVSPKIVEISDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 OY 181 SEDEYLEIQGITREQSGDYECASNDVAAPVVRVKVTYVNPYPISEAKGTGVPVGQGT 240
 DB 181 SEDEYLEIQGITREQSGDYECASNDVAAPVVRVKVTYVNPYPISEAKGTGVPVGQGT 240
 OY 241 LOCEASAVPSAEQWTKDKRLIEGKGVKNRPFSLKLIFFNYSYHDIYNYTCVASNK 300
 DB 241 LOCEASAVPSAEQWTKDKRLIEGKGVKNRPFSLKLIFFNYSYHDIYNYTCVASNK 300
 OY 301 LGHTNASIMLFGPGAVSEVSNCTSRAGCVWLLPLLVLLHLLKF 344
 DB 301 LGHTNASIMLFGPGAVSEVSNCTSRAGCVWLLPLLVLLHLLKF 344

RESULT 11
 ABU67162
 ID ABU67162 standard; Protein; 344 AA.
 XX AC ABU67162;
 XX DT 28-MAY-2003 (first entry)
 XX

PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866026.
 PR 01-JUN-2001; 2001US-0865034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0882636.
 PR 21-JUN-2001; 2001US-0886342.
 PR 18-JUL-2001; 2001US-0887879.
 PR 06-AUG-2001; 2001US-0908827.
 PR 09-AUG-2001; 2001US-0924419.
 PR 16-AUG-2001; 2001US-0927796.
 PR 19-DEC-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-332040/31..
 DR N-PSDB; ACA03790.
 XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification
 XX
 PS Claim 12; Fig 376; 660pp; English.
 CC
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
 CC proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. AB066570-AB066844 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipdsIDentry.html.
 XX
 SQ Sequence 344 AA;
 Query Match 100.0%; Score 1806; DB 24; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTIQPKMNSISWAIFTGLAALCLFGVPSGDTAPKADNVTYRQGESATLRTID 60
 DB 1 MKTIQPKMNSISWAIFTGLAALCLFGVPSGDTAPKADNVTYRQGESATLRTID 60
 QY 61 NRVTWAWLNRSTILYAGNDKWCIDPRVLLSNTQTSIEIQNVVDYDGPYTSQVTD 120
 DB 61 NRVTWAWLNRSTILYAGNDKWCIDPRVLLSNTQTSIEIQNVVDYDGPYTSQVTD 120
 QY 121 NHPKTSRVHLIVQVSPKIVEISSINEGNNISLFTCTATGRPEPTVWHRHISPKAVGFV 180
 DB 121 NHPKTSRVHLIVQVSPKIVEISSINEGNNISLFTCTATGRPEPTVWHRHISPKAVGFV 180
 QY 181 SEDEYLEIOGIREQSGDYECASNDVAAPVRRVKVTVNYPPISEAKGTGYPVQKGT 240
 DB 181 SEDEYLEIOGIREQSGDYECASNDVAAPVRRVKVTVNYPPISEAKGTGYPVQKGT 240

QY 241 LOCASAVPSAEQWYKDDKRLIECKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 DB 241 LOCASAVPSAEQWYKDDKRLIECKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 QY 301 LGHTNASIMLFGCGAVSEVSNGTSSRACGCVWLLPLLVLLHLLKF 344
 DB 301 LGHTNASIMLFGCGAVSEVSNGTSSRACGCVWLLPLLVLLHLLKF 344

RESULT 10
 ABU67033
 ID ABU67033 standard; Protein; 344 AA.
 XX
 AC ABU67033;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 XX Human secreted/transmembrane, PRO, protein SEQ ID 376.
 DE Human; secreted protein; transmembrane protein; PRO;
 XX
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX
 XX Homo sapiens.
 OS
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05930.
 PR 12-JUN-1996; 96WO-US12456.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19337.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 20-NOV-1998; 98WO-US22992.
 PR 01-DEC-1998; 98WO-US24855.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.

QY 181. SEDEYLETQITRSGSDYECASNDVAAPVVRVVKVTVNPPYI5EAKGTGVPVQKGT 240
 DB 181 SEDEYLETQITRSGSDYECASNDVAAPVVRVVKVTVNPPYI5EAKGTGVPVQKGT 240
 QY 241. LOCEASAPVSAEFQYKDDRLIEGKKGKVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
 DB 241 LOCEASAPVSAEFQYKDDRLIEGKKGKVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
 QY 301 LGHTNASIMLFGPGAVSEVSGTSRRAGCVWLLPLLVLHLLKLF 344
 DB 301 LGHTNASIMLFGPGAVSEVSGTSRRAGCVWLLPLLVLHLLKLF 344

RESULT 8
 ABU72061
 ID ABU72061 standard; Protein; 344 AA.
 AC ABU72061;
 XX
 DT 11-JUN-2003 (first entry)
 DE Novel human, secreted and transmembrane protein PRO337.
 XX
 KW Human; secreted and transmembrane polypeptide; PRO;
 KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
 KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
 KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
 KW toxin; radiolabel; antibody; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tissue typing.
 XX
 OS Homo sapiens.
 XX
 PN US2002177165-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 01-FEB-2002; 2002US-0066500.
 XX
 PR 14-JUL-1998; 98WO-US14552.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 20-NOV-1998; 98WO-US24855.
 PR 25-NOV-1998; 98WO-US25190.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-MAR-1999; 98WO-US05028.
 PR 02-JUN-1999; 98WO-US22252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20394.
 PR 15-SEP-1999; 98WO-US21090.
 PR 15-SEP-1999; 98WO-US21547.
 PR 30-NOV-1999; 98WO-US28313.
 PR 01-DEC-1999; 98WO-US28301.
 PR 02-DEC-1999; 98WO-US28565.
 PR 15-DEC-1999; 98WO-US30999.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 09-MAR-2000; 2000WO-US06471.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 15-MAY-2000; 2000WO-US13358.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15284.
 PR 11-AUG-2000; 2000WO-US22031.

PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23528.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 26-AUG-1997; 97US-056974P.
 PR 17-SEP-1997; 97US-059115P.
 PR 18-SEP-1997; 97US-059263P.
 PR 19-SEP-1997; 97US-059588P.
 PR 17-OCT-1997; 97US-062285P.
 PR 24-OCT-1997; 97US-062816P.
 PR 27-OCT-1997; 97US-063082P.
 PR 29-OCT-1997; 97US-063329P.
 PR 21-NOV-1997; 97US-063733P.
 PR 25-NOV-1997; 97US-066364P.
 PR 16-DEC-1997; 97US-066840P.
 PR 09-FEB-1998; 97US-069694P.
 PR 09-FEB-1998; 98US-074086P.
 PR 25-MAR-1998; 98US-074092P.
 PR 08-APR-1998; 98US-079294P.
 PR 10-AUG-1998; 98US-081049P.
 PR 18-AUG-1998; 98US-095988P.
 PR 09-SEP-1998; 98US-097000P.
 PR 10-SEP-1998; 98US-099601P.
 PR 10-SEP-1998; 98US-099803P.
 PR 10-SEP-1998; 98US-099811P.
 PR 17-SEP-1998; 98US-099812P.
 PR 24-SEP-1998; 98US-100858P.
 PR 28-OCT-1998; 98US-101922P.
 PR 20-NOV-1998; 98US-106032P.
 PR 23-MAR-1999; 98US-109304P.
 PR 15-JUN-1999; 98US-125778P.
 PR 20-JUL-1999; 98US-139695P.
 PR 26-JUL-1999; 98US-145070P.
 PR 17-AUG-1999; 98US-145698P.
 PR 07-DEC-1999; 98US-149396P.
 PR 15-NOV-2001; 2001US-0002796.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashtenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gao W, Gerber H, Garritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JF, Napier MA, Pan J,
 PI Pooni NF, Roy MA, Stewart JA, Tumas D, Watanabe CK, Williams PM,
 PI Wood WI, Zhang Z;
 XX
 DR WPI; 2003-328482/31.
 DR N-PSDB; ACA60526...

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, for identifying agonists or antagonists of polypeptide, and as molecular weight markers

Claim 12; Fig 52; 254pp; English.

The invention describes an isolated, secreted and transmembrane polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a cell expressing the above polypeptides. The bioactive molecule, a toxin, radiolabel or an antibody, causes cell death. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. The polynucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 11; Fig 56; 565pp; English.
 PS
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABL88417 to
 CC ABL885003. The PRO proteins and polynucleotides have cardiac, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88249 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 XX Sequence 344 AA;
 Query Match 100.0%; Score 1806; DB 23; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTTPKMHNSISWAFITGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
 DB 1 MKTTPKMHNSISWAFITGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
 QY 61 NRVTRVAVLNRSTILYAGNDKWCCLDPRVLLSNTQYISIEIONVDYDGPYTCVQTD 120
 DB 61 NRVTRVAVLNRSTILYAGNDKWCCLDPRVLLSNTQYISIEIONVDYDGPYTCVQTD 120
 QY 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGV 180
 DB 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGV 180
 QY 181 SEDEYLEIOGITREQSGDYECASNDVAAPVRRVKTVYVPPYISEAKGTGVPVQKGT 240
 DB 181 SEDEYLEIOGITREQSGDYECASNDVAAPVRRVKTVYVPPYISEAKGTGVPVQKGT 240
 QY 241 LOCEASAVPSAEQWYKDDKRLIEGKGVKVENRPLSKLFFNVSEHDYGVNTCVASNK 300
 DB 241 LOCEASAVPSAEQWYKDDKRLIEGKGVKVENRPLSKLFFNVSEHDYGVNTCVASNK 300
 QY 301 LGHTNASIMLFGGAVSEVSNGTSTRACGVWLLPLVLLHLK 344
 DB 301 LGHTNASIMLFGGAVSEVSNGTSTRACGVWLLPLVLLHLK 344
 RESULT 7
 ID AU083654
 XX AU083654 standard; Protein; 344 AA.
 XX AU083654;
 XX
 DT 08-MAY-2002 (first entry)
 DE Human PRO protein, Seq ID No 126.
 DE
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 XX WO200208288-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX PD
 XX

PF 29-JUN-2001; 2001WO-US21066.
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220621F.
 PR 25-JUL-2000; 2000US-220624F.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 26-JUL-2000; 2000US-220693P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX (GETH) GENENTECH INC.
 XX
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2002-172001/22.
 DR N-PSDB; ABK33598.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO-related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour.
 XX
 XX Claim 11; Figure 126; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression in, pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention.
 XX
 XX Sequence 344 AA;
 Query Match 100.0%; Score 1806; DB 23; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTTPKMHNSISWAFITGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
 DB 1 MKTTPKMHNSISWAFITGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
 QY 61 NRVTRVAVLNRSTILYAGNDKWCCLDPRVLLSNTQYISIEIONVDYDGPYTCVQTD 120
 DB 61 NRVTRVAVLNRSTILYAGNDKWCCLDPRVLLSNTQYISIEIONVDYDGPYTCVQTD 120
 QY 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGV 180
 DB 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGV 180

```

PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US15692.
PR 28-JUN-2001; 2001WO-US00000.
XX
XX (GETH ) GENENTECH INC.
PA (BAKER) BAKER K P.
PA (FERR) FERRARA N.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANJ) PAN J.
PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-171999/22.
XX N-PSDB; ABL95588.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal
XX
XX Claim 11; Fig 56; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX cardiovascular, endothelial or angiogenic disorder, including cardiac
XX hyperthrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The present sequence is a PRO protein of the invention.
XX
XX Sequence 344 AA;
XX
XX Query Match 100.0%; Score 1806; DB 23; Length 344;
XX Best Local Similarity 100.0%; Pred. No. 3e-149;
XX Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MKTIQPMHNSWALFTGLAALCLFQGVVPSGDATPKAMDNVTVROGESATLRCTID 60
XX DB 1 MKTIQPMHNSWALFTGLAALCLFQGVVPSGDATPKAMDNVTVROGESATLRCTID 60
XX
XX QY 61 NRTVRVAVLNRSITLYAGNDKWLDPVLLSNTQTSIEIQNVNDYDEGPTCSVQTD 120
XX DB 61 NRTVRVAVLNRSITLYAGNDKWLDPVLLSNTQTSIEIQNVNDYDEGPTCSVQTD 120
XX
XX QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTICATGRPEPTVTRHISPKAVGFV 180
XX DB 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTICATGRPEPTVTRHISPKAVGFV 180
XX
XX QY 181 SEDEYLEIQIGITREQSGDYECASNDVAAPVRRVKKVTVNPPYISEAKGTGVPVQKGT 240
XX DB 181 SEDEYLEIQIGITREQSGDYECASNDVAAPVRRVKKVTVNPPYISEAKGTGVPVQKGT 240
XX
XX QY 241 LOCEASAVPSAEFQWKDDKELTEGKGVKVENRPFSLKLIFFNVSHDYGNVTCVSNK 300
XX DB 241 LOCEASAVPSAEFQWKDDKELTEGKGVKVENRPFSLKLIFFNVSHDYGNVTCVSNK 300
XX
XX QY 301 LGHTNASIMLFGPGAVSEVSNGTSTRAGCVWLLPLLVHLHLK 344
XX DB 301 LGHTNASIMLFGPGAVSEVSNGTSTRAGCVWLLPLLVHLHLK 344

```

RESULT 6

ABB84844 standard; Protein; 344 AA.

XX ABB84844;

XX 16-MAY-2002 (first entry)

XX Human PRO337 protein sequence SEQ ID NO:56.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;

XX vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

XX age-related macular degeneration; arterial restenosis; angina;

XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;

XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

XX wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US19692.

XX 23-JUN-2000; 2000US-213637P.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220664P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 24-AUG-2000; 2000WO-US23328.

XX 07-SEP-2000; 2000US-230978P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 10-NOV-2000; 2000WO-US30952.

XX 01-DEC-2000; 2000WO-US30873.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 01-MAR-2001; 2001WO-US06520.

XX 03-MAR-2001; 2001WO-US06666.

XX 14-MAR-2001; 2001US-0808689.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 30-MAY-2001; 2001WO-US17092.

XX 30-MAY-2001; 2001US-0870574.

XX 01-JUN-2001; 2001WO-US17443.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.

XX N-PSDB; ABL88099.

XX

XX 15-JUN-1999; 99US-0139695.
 PR 20-JUL-1999; 99US-0145070.
 PR 26-JUL-1999; 99US-0145698.
 PR 17-AUG-1999; 99US-0149396.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.
 PR 07-DEC-1999; 99US-0169495.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05941.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 15-MAY-2000; 2000WO-US13358.
 PR 17-MAY-2000; 2000WO-US13705.
 XX
 PA (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski P, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
 PI Wood WI, Zhang Z;
 XX
 DR WPI: 2001-050091/06.
 DR N-PSDB; AAC87037.
 XX
 PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
 PT transmembrane polypeptide is useful for gene therapy and identification
 PT of related polypeptides -
 XX
 XX Claim 12: Fig 52: 244pp; English.
 XX
 CC The present sequence represents a human secreted and transmembrane
 CC polypeptide. The specification describes human polypeptides, designated
 CC PRO196, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
 CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
 CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
 CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
 CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
 CC can be modulated with agents that bind to these polypeptides, resulting
 CC in the death of the cells. The polynucleotides encoding these
 CC polypeptides are useful in the recombinant production of the
 CC polypeptides, as a hybridisation probe to screen libraries to isolate
 CC homologous sequences, or to map the gene. They may also be used for
 CC analysing genetic disorders, and to produce transgenic animals which are
 CC useful for the development and screening of therapeutically useful
 CC reagents. The polynucleotides can also be used in gene therapy e.g. to
 CC replace a defective gene.
 XX
 SU Sequence 344 AA:
 Query Match 100.0%; Score 1806; DB.22: Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MKTIQPMHNSISWALFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQESATLACTID 60
 DB 1 MKTIQPMHNSISWALFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQESATLACTID 60
 OY 61 NRVTRVAVLNRSITLYAGNDKCLDPRVLLSTQYVSIQNVYDVGPTCSVQTD 120
 DB 61 NRVTRVAVLNRSITLYAGNDKCLDPRVLLSTQYVSIQNVYDVGPTCSVQTD 120
 OY 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180

DB 121 NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 OY 181 SEDEYLEIOGITREQSGDYECASANDVAAPVYRRVYKVTNVPYVISEAKGTGVPVQKGT 240
 DB 181 SEDEYLEIOGITREQSGDYECASANDVAAPVYRRVYKVTNVPYVISEAKGTGVPVQKGT 240
 OY 241 LQCEASAVPSAEFQYKDDKRLLEGKKGKVENREPLSKLIFFNVSEHDYGNVTCVASK 300
 DB 241 LQCEASAVPSAEFQYKDDKRLLEGKKGKVENREPLSKLIFFNVSEHDYGNVTCVASK 300
 OY 301 LGHTNASIMLFGPGAVSEVNGTSRRAGCVWLLPLLVLLHLKLF 344
 DB 301 LGHTNASIMLFGPGAVSEVNGTSRRAGCVWLLPLLVLLHLKLF 344

RESULT 5

AB95450
 ID AB95450 standard; Protein: 344 AA.

XX
 AC AB95450;

XX
 DT 19-JUL-2002 (first entry)

XX
 DE Human angiogenesis related protein PRO337 SEQ ID NO: 56.

XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cytostatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.

XX
 OS Homo sapiens.

XX
 PN WO200208284-A2.

XX
 PD 31-JAN-2002.

XX
 PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-064367.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 10-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US30873.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806899.
 PR 22-MAR-2001; 2001US-0816244.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 30-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.

AAU12359
 ID AAU12359 standard; Protein; 344 AA.
 AC AAU12359;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO337 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z.
 XX
 DR NPI: 2001-408281/43.
 DR W-PSDB: AAS21431.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical.
 XX
 PS Claim 12; Fig 376; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.

CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals, and can be used in gene therapy.
 XX
 SQ Sequence 344 AA;
 Query Match 100.0%; Score 1806; DB 22; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTIQPKMNSISWAIETGLAALCLFQGVPRVSGDATFPKANDVTVRGGSATLRCTID 60
 DB 1 MKTIQPKMNSISWAIETGLAALCLFQGVPRVSGDATFPKANDVTVRGGSATLRCTID 60
 QY 61 NRVTRVAVLNBSITLYAGNDKCLDPVLLSNTOYSTEIONVDVDEGPTCSVQTD 120
 DB 61 NRVTRVAVLNBSITLYAGNDKCLDPVLLSNTOYSTEIONVDVDEGPTCSVQTD 120
 QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPRKGVFV 180
 DB 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPRKGVFV 180
 QY 181 SEDEYLEIQITRQSGDYECASNDVAAPVVRKVTYVVPYPISEAKGTGVPVGQKGT 240
 DB 181 SEDEYLEIQITRQSGDYECASNDVAAPVVRKVTYVVPYPISEAKGTGVPVGQKGT 240
 QY 241 LQCEASAVPSAEFQWYKDKRLTEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
 DB 241 LQCEASAVPSAEFQWYKDKRLTEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
 QY 301 LGHTNASIMLFGPGAVSEVSNGTSSRRACGVLLPLLVLLHLLAKF 344
 DB 301 LGHTNASIMLFGPGAVSEVSNGTSSRRACGVLLPLLVLLHLLAKF 344
 RESULT 4
 AAB31204
 ID AAB31204 standard; Protein; 344 AA.
 AC AAB31204;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Amino acid sequence of human polypeptide PRO337.
 XX
 KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
 KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
 KW PRO1183; PRO1272; PRO1419; PRO4999; PRO170; PRO248; PRO353; PRO1318;
 KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
 KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..28
 FT /note="signal peptide"
 PN WO200077037-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 22-MAY-2000; 2000WO-US14042.

PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 XX (GETH) GENENTECH INC.
 XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Geo W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX NPI: 2000-611443/58.
 DR N-PSDB: AAC78590.
 XX
 XX Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities
 XX
 XX Claim 12; Fig 222; 636pp; English.
 XX
 XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides, for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 XX Sequence 344 AA;
 SQ
 Query Match 100.0%; Score 1806; DB 21; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTIQPKMHSISWAIFTGLAALCLFQGVPRVSGDATFPKAMDNVTVRQGESATLRCITD 60
 DB 1 MKTIQPKMHSISWAIFTGLAALCLFQGVPRVSGDATFPKAMDNVTVRQGESATLRCITD 60
 QY 61 NRVTAVLNRSTILYAGNDKWLCDPRVLLSNTQTSIEIQNVVDYDGPVTCVQTD 120
 DB 61 NRVTAVLNRSTILYAGNDKWLCDPRVLLSNTQTSIEIQNVVDYDGPVTCVQTD 120
 QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 DB 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 QY 181 SEDEYLEIQGITREGSGDYECASNDVAAPVVRVKVTVNPPYIIEAKGTGVPVQKGT 240
 DB 181 SEDEYLEIQGITREGSGDYECASNDVAAPVVRVKVTVNPPYIIEAKGTGVPVQKGT 240
 QY 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKN 300
 DB 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKN 300
 QY 301 LGHTNASIMLFGPGAVSEVSGNSTRACGVWLLPLLLVHLLKLF 344
 DB 301 LGHTNASIMLFGPGAVSEVSGNSTRACGVWLLPLLLVHLLKLF 344
 RESULT 2
 ID ANY57601
 XX ANY57601 standard; Protein; 344 AA.
 XX
 AC ANY57601;

XX 10-MAR-2000 (first entry)
 DT
 XX
 DE Human protein SEQ.ID NO:1.
 XX
 XX Human; hematopoietic cell regulation; tissue generation; reparation;
 KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
 KW receptor; ligand; autumune; infection-related immunodeficiency;
 KW inflammatory disorder; neurological disease.
 XX
 XX Homo sapiens,
 OS
 PN WO9958668-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 13-MAY-1999; 99WO-JP02485.
 XX
 PR 14-MAY-1998; 98JP-0131815.
 XX
 PA (ONCOY) ONO PHARM CO LTD.
 XX
 PI Fukushima D, Shibayama S, Tada H;
 XX
 DR WPI; 2000-062298/05.
 DR N-PSDB; AA247892, AA247893.
 XX
 XX New polypeptides of human origin having cell-regulatory, tissue
 PT generation, coagulant and other activities
 PT
 PS Claim 1; Page 38-40; 84pp; Japanese.
 XX
 CC The present sequence represents a specifically claimed novel human
 CC protein. The novel human protein can be used in therapeutic drugs for
 CC the prevention and treatment of a broad range of disorders including
 CC autoimmune and infection-related immunodeficiency, inflammatory
 CC disorders, and neurological diseases. The novel protein is expected of
 CC having hematopoietic cell regulatory activity, tissue generation/
 CC reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
 CC blood coagulation and thrombus activity, and receptor/ligand activity.
 XX
 XX Sequence 344 AA;
 SQ
 Query Match 100.0%; Score 1806; DB 21; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3e-149;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTIQPKMHSISWAIFTGLAALCLFQGVPRVSGDATFPKAMDNVTVRQGESATLRCITD 60
 DB 1 MKTIQPKMHSISWAIFTGLAALCLFQGVPRVSGDATFPKAMDNVTVRQGESATLRCITD 60
 QY 61 NRVTAVLNRSTILYAGNDKWLCDPRVLLSNTQTSIEIQNVVDYDGPVTCVQTD 120
 DB 61 NRVTAVLNRSTILYAGNDKWLCDPRVLLSNTQTSIEIQNVVDYDGPVTCVQTD 120
 QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 DB 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
 QY 181 SEDEYLEIQGITREGSGDYECASNDVAAPVVRVKVTVNPPYIIEAKGTGVPVQKGT 240
 DB 181 SEDEYLEIQGITREGSGDYECASNDVAAPVVRVKVTVNPPYIIEAKGTGVPVQKGT 240
 QY 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKN 300
 DB 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKN 300
 QY 301 LGHTNASIMLFGPGAVSEVSGNSTRACGVWLLPLLLVHLLKLF 344
 DB 301 LGHTNASIMLFGPGAVSEVSGNSTRACGVWLLPLLLVHLLKLF 344
 RESULT 3

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 02:49:08 ; Search time 72 Seconds
(without alignments)
758.360 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 1806

Sequence: 1 MKTIQPKMHSISWAIFTGL.....RRAGCVLLPLDLVLLKLF 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	100.0	344	21	Human PRO337 prote
2	1806	100.0	344	21	Human protein SEQ
3	1806	100.0	344	22	Human PRO337 polyp
4	1806	100.0	344	22	Amino acid sequenc
5	1806	100.0	344	23	Human androgenesis
6	1806	100.0	344	23	Human PRO337 prote
7	1806	100.0	344	23	Human PRO protein,
8	1806	100.0	344	24	Novel human secret
9	1806	100.0	344	24	Human PRO polypept

10	1806	100.0	344	24	ABU67033	Human secreted/tra
11	1806	100.0	344	24	ABU67162	Novel human secret
12	1806	100.0	344	24	ABU67293	Novel human secret
13	1806	100.0	344	24	ABUS9838	Novel secreted and
14	1806	100.0	344	24	ABU61159	Human PRO337 polyp
15	1806	100.0	355	22	AAU40459	Human polypeptide
16	1799	99.6	344	21	AAU19721	Human SECX Clone 1
17	1799	99.6	344	21	AAU19722	Human PRO337 prote
18	1791.5	99.2	343	20	AAU1773	Human PRO337 prote
19	1665.5	92.2	344	22	AAU38713	Human polypeptide
20	1665.5	92.2	344	24	ABU56719	Lung cancer-associ
21	1643	91.0	381	23	AAU79205	Human kruppel asso
22	1642	90.9	313	21	AAU57602	Human protein SEQ
23	932.5	51.6	335	23	AAU19641	Human limbic syste
24	926.5	51.3	338	17	AAU05153	Rat LAMP residues
25	926.5	51.3	338	17	AAU05154	Rat LAMP residues
26	923.5	51.1	325	17	AAU05152	Human LAMP residue
27	913	50.6	361	17	AAU05172	Rat LAMP clone 6c
28	908	50.3	308	17	AAU05157	Human LAMP residues
29	907	50.2	315	17	AAU05158	Rat LAMP residues
30	905	50.1	310	17	AAU05156	Rat mature LAMP
31	902	49.9	304	17	AAU05155	Human mature LAMP
32	893	49.4	383	24	ABR39441	Human GENSET polyp
33	886.5	49.1	287	17	AAU05159	Human LAMP residue
34	885.5	49.0	287	17	AAU05160	Rat LAMP residues
35	852.5	47.2	326	22	AAU75020	Human colon cancer
36	823	45.6	344	22	AAU1212	Amino acid sequenc
37	823	45.6	344	23	AAU33580	Human NOV12a prote
38	823	45.6	354	23	AAU33592	Human PRO protein,
39	823	45.6	354	24	ABU72069	Novel human secret
40	823	45.6	354	24	ABU67170	Novel human secret
41	823	45.6	354	24	ABU67301	Novel human secret
42	822	45.5	354	23	ABU96407	Human NOV6, KILON
43	819	45.3	354	23	ABU53581	Human NOV12b prote
44	815	45.1	352	21	AAU44331	Human PRO4993 prot
45	815	45.1	352	24	ABU61161	Human PRO4993 poly

ALIGNMENTS

RESULT 1

AAU44329
ID AAB44329 standard; Protein; 344 AA.

AC AAB44329;

DT 08-FEB-2001 (first entry)

DE Human PRO337 protein sequence SEQ ID NO:523.

XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX expressed sequence tag; detection; cancer.

OS Homo sapiens.

PN W0200053756-A2.

XX 14-SEP-2000.

PF 18-FEB-2000; 2000WO-US04341.

XX 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 23-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PRIOR APPLICATION NUMBER: 60/081203	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09
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100.0%			

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QY		
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DB		
121	AGAAAATAATCATGAATAACCATCAGCCAAAATGCAAAATCTATCTCTTGCGCAAT	180
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121	AGAAAATAATCATGAATAACCATCAGCCAAAATGCAAAATCTATCTCTTGCGCAAT	180
DB		
181	CTTCACGGCGTGGTCTGTGTCTCTTCACAGAGATGCCGTGCCAGCGAGATGC	240
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181	CTTCACGGCGTGGTCTGTGTCTCTTCACAGAGATGCCGTGCCAGCGAGATGC	240
DB		
241	CACCTCTCCCAAAAGCTATGACAACGTGAGGGTGGCGAGGGGAGAGCGCCACCCCTCAG	300
QY		
241	CACCTCTCCCAAAAGCTATGACAACGTGAGGGTGGCGAGGGGAGAGCGCCACCCCTCAG	300
DB		
301	GTGCATCTATTGACAACCGGGTACACCGGGTGCGCTGAACCGCAGCAGCATCTCTCTA	360
QY		
301	GTGCATCTATTGACAACCGGGTACACCGGGTGCGCTGAACCGCAGCAGCATCTCTCTA	360
DB		
361	TCCTGGGAATGACAAGTGGTGCCCTGGATCCCTCGGTGGTCTCTTGAGCAACACCCAAAC	420
QY		
361	TCCTGGGAATGACAAGTGGTGCCCTGGATCCCTCGGTGGTCTCTTGAGCAACACCCAAAC	420
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QY		
421	GCAGTACAGCATCGAGATCCGAACGCTGGATGTGTATGACGAGGGCCCTTACACCTGCTC	480
DB		
481	GGTGCAGACAGAACACCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540
QY		
481	GGTGCAGACAGAACACCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540
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541	CAAAATGTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600
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QY		
661	GTTTGGCTTTGTGATGAAGACGAATACTTTGAAATTCAGGGCATCACCCGGGAGCAGCTC	720
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 DB 1321 AAGAAATACCTTTGGGGGGAAGAGTTTAAAGAAAGAAATTTGAAATTTGCTTGCAGATA 1380
 OY 1381 TTAGGTACAAATGGAGTTTCTTTTCCCAACGGGAAGAACACACACCCCGGCTTGA 1440
 DB 1381 TTAGGTACAAATGGAGTTTCTTTTCCCAACGGGAAGAACACACACCCCGGCTTGA 1440
 OY 1441 CCCACTGCAAGTGCATCGTCAACCTCTTTTGTGCTGCCAGTGTGGCAAGGGCTTCAGCCTC 1500
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RESULT 15

US-09-978-423A-522

; Sequence 522, Application US/0978423A

; Publication No. US20030069178A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630PIC21

; CURRENT APPLICATION NUMBER: US/09/978,423A

; CURRENT FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
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 PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 1679; DB 11; Length 1679;
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 481 GGTGACAGACAGACACCCAGACCTCTAGGTCACCTGATGATGATGATGATGATGATGATGAT 540
 541 CAAAATTTGATGATTTCTGATATCTCCATTAATGAAGGACATATATAGCTTCAC 600
 541 CAAAATTTGATGATTTCTGATATCTCCATTAATGAAGGACATATATAGCTTCAC 600
 601 CTGCATAGCACTGTTAGACAGACCTACCGTTACTTGGAGACACATCTCTCCCAANG 660
 601 CTGCATAGCACTGTTAGACAGACCTACCGTTACTTGGAGACACATCTCTCCCAANG 660
 661 GTTGCTTTGTGAGTGAAGACGAATCTTGAATTTAGGGCATCAACCCGGGAGCAGTC 720
 661 GTTGCTTTGTGAGTGAAGACGAATCTTGAATTTAGGGCATCAACCCGGGAGCAGTC 720
 721 AGGGGACTACGAGTGCAGTCCCTCCAATGACGTGGCGCGCGCGCGCGCGCGCGCGCGCG 780
 721 AGGGGACTACGAGTGCAGTCCCTCCAATGACGTGGCGCGCGCGCGCGCGCGCGCGCGCG 780
 781 GGTCAACCTGAACCTATCCACCATACATTTGAGAGCAAGGGGTACAGGTGTCCTGGG 840
 781 GGTCAACCTGAACCTATCCACCATACATTTGAGAGCAAGGGGTACAGGTGTCCTGGG 840
 841 ACAGAGGGGACACTGACGTGTAAGCTCTAGAGCTCCCTCAGAGATTTCCAGTGGTA 900
 841 ACAGAGGGGACACTGACGTGTAAGCTCTAGAGCTCCCTCAGAGATTTCCAGTGGTA 900
 901 CAGGATGACAAAAGACTGATTAAGAGAAAGAGGGGTGAAGTGGAAAAACAGACCTTT 960
 901 CAGGATGACAAAAGACTGATTAAGAGAAAGAGGGGTGAAGTGGAAAAACAGACCTTT 960
 961 CTTCTCAAAACTCATCTTCAATGCTGTAACATGACTATGGGAACTACACTTCGCT 1020
 961 CTTCTCAAAACTCATCTTCAATGCTGTAACATGACTATGGGAACTACACTTCGCT 1020
 1021 GGCCTCAAAAGCTGGGCGACACCAATGCCAGCATCTGCTATTGGTGGAGCGCGCT 1080
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1561	Cy	GTCCATAGAGAGCAACAGATGAGACTTCCGGCCCAAGCGTGCGCTCGGGCACTTGG	1620
1561	Db	GTCCATAGAGAGCAACAGATGAGACTTCCGGCCCAAGCGTGCGCTCGGGCACTTGG	1620
1621	Qy	GTGACTGTGCCACCACCGGGCTGTGTGTGAACCTGAAATATAAAAGACAAAAAAA	1679
1621	Db	GTGACTGTGCCACCACCGGGCTGTGTGTGAACCTGAAATATAAAAGACAAAAAAA	1679

RESULT 14

US-RESOL-918-585A-522

Sequence 522, Application US/09918585A
Publication No. US20030060406A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Bensoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filizvoff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter E.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmitted
FILE REFERENCE: P2830P1C1

CURRENT APPLICATION NUMBER: US/09/918585A
CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/0632250
PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/0636364
PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20

[illegible]

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC14
CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06

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: PRIOR APPLICATION NUMBER: 60/085579
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085580
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085573
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085704
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085697

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Query Match	100.08;	Score 1679;	DB 11;	Length 1679;
Best Local Similarity	100.04;	Pred. No. 0;		
Matches 1679;	Conservative	0;	Mismatches	0;
			Indels	Gaps
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DB	1	GTGTGTCTTCAGCAAAACAGTGGATTTAAATCTCTTCGACACAGCTTGAGACCAAC	60	
QY	61	ATCTCTACGAGAAAGAAAGAAAGAAACCGACCTGCAATATAAGAAAGAAAGAAAGAG	120	
DB	61	ATCTCTACGAGAAAGAAAGAAAGAAACCGACCTGCAATATAAGAAAGAAAGAAAGAG	120	
QY	121	AGAAAAAAATCTGAAAAACCATCCAGCCAAAATATGCATTTCTATCTCTTGGGCAT	180	
DB	121	AGAAAAAAATCTGAAAAACCATCCAGCCAAAATATGCATTTCTATCTCTTGGGCAT	180	
QY	181	CTTCACGGGCTGGCTGTCTGTCTCTTCACAGGAGTCCCGTGGCCGACGGAGATGC	240	
DB	181	CTTCACGGGCTGGCTGTCTGTCTCTTCACAGGAGTCCCGTGGCCGACGGAGATGC	240	
QY	241	CACCTTCCCAAGCATGTGACACAGTGACGGTCCGCGAGGGGAGACGCCACCCCTCAG	300	
DB	241	CACCTTCCCAAGCATGTGACACAGTGACGGTCCGCGAGGGGAGACGCCACCCCTCAG	300	
QY	301	GTGCATCTTGAACAACCGGCTACCCGGGTGGCCCTGGCTAAACCGACGACCATTCCTCTA	360	
DB	301	GTGCATCTTGAACAACCGGCTACCCGGGTGGCCCTGGCTAAACCGACGACCATTCCTCTA	360	
QY	361	TGCTGGGAATGACAGTGGTGGCTGAGATCCCTGGTGGTCTCTTCGACGACACCCCAAC	420	
DB	361	TGCTGGGAATGACAGTGGTGGCTGAGATCCCTGGTGGTCTCTTCGACGACACCCCAAC	420	
QY	421	GCAGTACAGCATCGAGATCAGAACGTGATGTATGACGAGGGCCCTACACCTGCTC	480	
DB	421	GCAGTACAGCATCGAGATCAGAACGTGATGTATGACGAGGGCCCTACACCTGCTC	480	
QY	481	GGTGACAGACACACACCCAAAGACCTCTAGGGTCCACCTCATTTGGCAATCTCC	540	
DB	481	GGTGACAGACACACACCCAAAGACCTCTAGGGTCCACCTCATTTGGCAATCTCC	540	
QY	541	CAAAATGTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCTAC	600	
DB	541	CAAAATGTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCTAC	600	
QY	601	CTGCATAGCAACTGGTAGACACGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGC	660	
DB	601	CTGCATAGCAACTGGTAGACACGAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGC	660	
QY	661	GTTTGGCTTTGTGAGTGAAGAGAAATCTTTGGAATTCAGGGCATCATCCCGGAGCAGTCT	720	
DB	661	GTTTGGCTTTGTGAGTGAAGAGAAATCTTTGGAATTCAGGGCATCATCCCGGAGCAGTCT	720	
QY	721	AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCCGCGCCGCTGGTACGGAGAGTAA	780	
DB	721	AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCCGCGCCGCTGGTACGGAGAGTAA	780	
QY	781	GGTCACCGTGAACATATCCACCATACATTTTCAGAGCAAGGGGTACAGGTGTCGCCGTGGG	840	
DB	781	GGTCACCGTGAACATATCCACCATACATTTTCAGAGCAAGGGGTACAGGTGTCGCCGTGGG	840	
QY	841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACAGTGTA	900	
DB	841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACAGTGTA	900	

QY	901	CAAGGATGACAAAAGACTGATTCAAGGAAAGAAAGGGTGAAAGTGGAAAACAGACCTTT	960
DB	901	CAAGGATGACAAAAGACTGATTCAAGGAAAGAAAGGGTGAAAGTGGAAAACAGACCTTT	960
QY	961	CTCTCAAAAGCTCATCTCTTCAATGCTCTGAAACATGACTATGGGAACTACACTTCGCT	1020
DB	961	CTCTCAAAAGCTCATCTCTTCAATGCTCTGAAACATGACTATGGGAACTACACTTCGCT	1020
QY	1021	GGCTCCAAACAAAGCTGGGCCACACCAATGCCAGCAGCATCATGCTATTTTGGTCCAGGCGCGT	1080
DB	1021	GGCTCCAAACAAAGCTGGGCCACACCAATGCCAGCAGCATCATGCTATTTTGGTCCAGGCGCGT	1080
QY	1081	CAGCAGGTGAGCAACAGCGACGTCGAGAGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT	1140
DB	1081	CAGCAGGTGAGCAACAGCGACGTCGAGAGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT	1140
QY	1141	GGTCTGGACCTGCTTCTCAAATTTTGATGTGAGTGCACCTTCCCAACCCGGGAAAGGCT	1200
DB	1141	GGTCTGGACCTGCTTCTCAAATTTTGATGTGAGTGCACCTTCCCAACCCGGGAAAGGCT	1200
QY	1201	GC CGCACACACACACACACAGCAATGGCAACCCGACAGCAACCAATCAGATA	1260
DB	1201	GC CGCACACACACACACACAGCAATGGCAACCCGACAGCAACCAATCAGATA	1260
QY	1261	TATCAAAATGAAATTTAGAAGAAACACAGCCTCATGGCACAGAAATTTGAGGAGGGGAAC	1320
DB	1261	TATCAAAATGAAATTTAGAAGAAACACAGCCTCATGGCACAGAAATTTGAGGAGGGGAAC	1320
QY	1321	AAAGAAATCTTTGGGGGAAAAGAGTTTAAAAAAGAAATTTGAAATTTGCCTTCCAGATA	1380
DB	1321	AAAGAAATCTTTGGGGGAAAAGAGTTTAAAAAAGAAATTTGAAATTTGCCTTCCAGATA	1380
QY	1381	TTTAGTACAAATGGAGTTTTCTTTTCCAAACGGGAAAGAACACAGCACACCCGGCTTGA	1440
DB	1381	TTTAGTACAAATGGAGTTTTCTTTTCCAAACGGGAAAGAACACAGCACACCCGGCTTGA	1440
QY	1441	CCCACTGCAAGCTCATCTGTCGCAACCTCTTTGGTGCAGTGTGGGCAAGGCTCAGGCCTC	1500
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QY	1501	TC TGCCCAACAGAGTGCCCCACGCTGGAACATCTCTGGAGCTGGCCATTCGCCAAATTCATCA	1560
DB	1501	TC TGCCCAACAGAGTGCCCCACGCTGGAACATCTCTGGAGCTGGCCATTCGCCAAATTCATCA	1560
QY	1561	GTCCATPAGAGCAACAGAAATGAGACTTCCTCGGCGCCAAAGCGTGGCGCTCGCGGACCTTTCG	1620
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QY	1621	GTAGACTGTGCCACACCGCGCTGCTGTGTGAAACGCTGAAATTAAGAGAGCAAAAAAAA	1679
DB	1621	GTAGACTGTGCCACACCGCGCTGCTGTGTGAAACGCTGAAATTAAGAGAGCAAAAAAAA	1679

RESULT 13
US-978-924-522
Sequence 522, Application US/09978824
Publication No. US20030055216A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Grittsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher

PRIOR APPLICATION NUMBER:	60/077450
PRIOR FILING DATE:	1998-03-10
PRIOR APPLICATION NUMBER:	60/077632
PRIOR FILING DATE:	1998-03-11
PRIOR APPLICATION NUMBER:	60/077641
PRIOR FILING DATE:	1998-03-11
PRIOR APPLICATION NUMBER:	60/077649
PRIOR FILING DATE:	1998-03-11
PRIOR APPLICATION NUMBER:	60/077791
PRIOR FILING DATE:	1998-03-12
PRIOR APPLICATION NUMBER:	60/078004
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PRIOR APPLICATION NUMBER:	60/078886
PRIOR FILING DATE:	1998-03-20
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PRIOR APPLICATION NUMBER:	60/078939
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PRIOR APPLICATION NUMBER:	60/081952

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301 GTCCACTATGACAAACGGGTGACCCGGTGGCTGGCTAAACCGCAGCACCCTCTCTA 360
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301 GTCCACTATGACAAACGGGTGACCCGGTGGCTGGCTAAACCGCAGCACCCTCTCTA 360
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Db
361 TGCTGGGAATGACAAAGTGGTGGCTGGATCCTCGCGTGGTCTCTGAGCAACACCCAAAC 420
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421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGATGACGAGGGCCCTTACACCTGCTC 480
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Db
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QY
1261 TATACAAATGAAATTTAGAAAGAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAC 1320
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1261 TATACAAATGAAATTTAGAAAGAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAC 1320

RESULT 12

US-09-981-915A-522

Sequence 522, Application US/09981915A

Publication No. US20030054986A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

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APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P9630P1G12

CURRENT APPLICATION NUMBER: US/09/981,915A

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 11; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 GTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAACTTGAGACACAC 60
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 DB 121 AAAAAAAATCATGAAACCATCCAGCCAAATTCATCTTCTTGGGCAAT 180
 QY 181 CTTACGGGGCTGGTGTCTGTCTTCTTCCAGGAGTCCCGTGGCGAGATGC 240

Db 601 CTGATAGCACTGTAGACACAGAGCCTAGCGTTACTTGGAGACACATCTCTCCCAAGC 660
Qy 661 GGTTCGCTTGTGAGTGAAGACGAATCTTGGAAATCAGGGGCATACCCGGGAGCAGTC 720
Db 661 GGTTCGCTTGTGAGTGAAGACGAATCTTGGAAATCAGGGGCATACCCGGGAGCAGTC 720
Qy 721 AGGGACTACGAGTGCAGTGCCTTCCAAATGACGTGGCGGCCCGTGTGAGGAGATAAA 780
Db 721 AGGGACTACGAGTGCAGTGCCTTCCAAATGACGTGGCGGCCCGTGTGAGGAGATAAA 780
Qy 781 GGTACCCGTAATATCCACCACATATTCAGAACCAAGGGTACAGGTGTCCCGGTGG 840
Db 781 GGTACCCGTAATATCCACCACATATTCAGAACCAAGGGTACAGGTGTCCCGGTGG 840
Qy 841 AAAAAAGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGA 900
Db 841 AAAAAAGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGA 900
Qy 901 CAAGATGACAAAGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGAAACAGACCTTT 960
Db 901 CAAGATGACAAAGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGAAACAGACCTTT 960
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Db 961 CCTCTCAAACTCATCTTCTTCAATGTCTGAACATGACTATGGAACTACACTTGGGT 1020
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Db 1021 GGCTCTCAAGAGTGGGCGCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGT 1080
Qy 1081 CAGCGAGTGACCAACGCGCTGAGAGGCGCGCTGCTGCTGCTGCTGCTGCTCTCT 1140
Db 1081 CAGCGAGTGACCAACGCGCTGAGAGGCGCGCTGCTGCTGCTGCTGCTGCTCTCT 1140
Qy 1141 GGTCTGCACTGCTCTCAATTTGATGTGAGTGGCCACTTCCCGCCGCGGAAGGCT 1200
Db 1141 GGTCTGCACTGCTCTCAATTTGATGTGAGTGGCCACTTCCCGCCGCGGAAGGCT 1200
Qy 1201 GCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
Db 1201 GCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
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Sequence 522, Application US/09999833A
Publication No. US20030034405A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C85
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 08/918585
PRIOR FILING DATE: 2001-07-30/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Query Match      : 100.0% ; Score 1679; DB 11; Length 1679;
Best Local Similarity : 100.0% ; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGTGTCTTCAGCAAAACAGTGGATTTAAATCTCTTGCACAGCTGTGGAGGACAC 60
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QY      61 RATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
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QY      181 CTTACGGGGCTGGCTGCTGTGTCTTCTTCCAGAGAGTGCCTGCGCGAGGAGATGC 240
Db      181 CTTACGGGGCTGGCTGCTGTGTCTTCTTCCAGAGAGTGCCTGCGCGAGGAGATGC 240

QY      241 CACCTTCCCAAGCTATGAGCAACGTGACGGTCCGGAGGGGGAGAGCCGCCCTCAG 300
Db      241 CACCTTCCCAAGCTATGAGCAACGTGACGGTCCGGAGGGGGAGAGCCGCCCTCAG 300

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Db      301 GTGCACATATTGACAAACCGGGTCCACCGGGTGGCTTAAACCGAGCAGCATCTCTA 360

QY      361 TGCTGGGAATGACAAAGTGGTGCCTGGATCTCTCGGTGGTCTTCTGAGCAACCCAAAC 420
Db      361 TGCTGGGAATGACAAAGTGGTGCCTGGATCTCTCGGTGGTCTTCTGAGCAACCCAAAC 420

QY      421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
Db      421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

QY      481 GGTGACAGACCAACCCAGACCTCTAGGTCCACCTTATGAGGAGGAGGAGGAGGAGGAG 540
Db      481 GGTGACAGACCAACCCAGACCTCTAGGTCCACCTTATGAGGAGGAGGAGGAGGAGGAG 540

QY      541 CAAATTTGAGAGATTTCTTCAGATATCTCCATTTAATGAGGAGCAATATTAGCTCTAC 600
Db      541 CAAATTTGAGAGATTTCTTCAGATATCTCCATTTAATGAGGAGCAATATTAGCTCTAC 600

QY      601 CTGCTAGCAACTGTGTAGACAGGAGCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
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RESULT 10

US-09-978-564A-522
 ; Sequence 522, Application US/09978564A
 ; Publication No. US20030050241A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
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 ; APPLICANT: Fong, Sherman
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 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C25
 ; CURRENT APPLICATION NUMBER: US/09/978,564A
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
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 ; PRIOR FILING DATE: 1998-04-08

[illegible]

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DB 1501 TCTGCCACAGAGTGCCTCCACACGTGGAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
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DB 1621 GTAGCTGTGCCACACACGGCGTGTGTGTGAAACCTGAAATATAAAGAGCAAAAAAAA 1679
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US-09-978-403A-522
Sequence 522: Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC17
CURRENT APPLICATION NUMBER: US/09/978,403A
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-04-22

APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-04-29

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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C15
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SPO ID NO 522
LENGTH: 1679
TYPE: DNA
ORGANISM: Homo sapiens
US-09-978-585A-522

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Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy
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421 GCAGTACAGCATCGAGATCCAGAACTGATGATGATGATGATGATGATGATGATGATG 480
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Db
541 CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAGGAAAGAAATTAAGCTAC 600
Qy
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721 AGGGGACTACGAGTGCCTCCAAATGACGTGGCGCGCGCTGGTGGAGAGATATA 780
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721 AGGGGACTACGAGTGCCTCCAAATGACGTGGCGCGCGCTGGTGGAGAGATATA 780
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781 GGTACCGGTGAACATATCCACCATATTTCCAGAAAGGAGTACAGGTGTCCCGTGG 840

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Db 841 AAAAAAGGGGAGCTGTCAGTGTGAAGCTTCAGAGTCCCTTCAGAGAGAAATTCAGTGGTA 900
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Db 901 CAAGATACAAAAAGACTGATTGAAGAAAGAAAGGGGTGAAGTGGAAAGACAGACCTTT 960
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Db 1021 GGCCTCCACAGCTGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
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Db 1261 TATACAAATGAATATTAGAGAAACAGAGCTTAAAGAAAGAAATTTGAAATTTGCTTGCAGATA 1380
Qy 1321 AAGAAATACTTTGGGGGAAAGAGTAAAGAAAGAAATTTGAAATTTGCTTGCAGATA 1380
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RESULT 8

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US-09-978-191A-522
; Sequence 522, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrata, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

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Query Match				100.0%; Score 1679; DB 11; Length 1679;			
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QY	901	CAAGGATCAGAAAGACTGATTAAGGAAGAAAGGGGTGAAAGTGGAAACACAGACCTTT	960				
DB	901	CAAGGATCAGAAAGACTGATTAAGGAAGAAAGGGGTGAAAGTGGAAACACAGACCTTT	960				
QY	961	CCTCTCAAACTCATCTTCTCAATGTCTCTGACATGACTATGGGAACACTACCTTCGCT	1020				
DB	961	CCTCTCAAACTCATCTTCTCAATGTCTCTGACATGACTATGGGAACACTACCTTCGCT	1020				
QY	1021	GGCTCCCAACAGCTGGGCCACACCAACCAATGCCAGCATCATCTATTTGGTCCAGGGCGGT	1080				

DB	1021	GGCTCCCAACAGCTGGGCCACCAATGCCAGCATCATCTATTTGGTCCAGGGCGGT	1080				
QY	1081	CAGGAGGTGAGCAACAGCGCAGTGGAGGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140				
DB	1081	CAGGAGGTGAGCAACAGCGCAGTGGAGGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140				
QY	1141	GCTCTTGCACCTCTCTCAAAATTTGATGTAGTGCCACTTCCGCCAGGGGAAAGGCT	1200				
DB	1141	GCTCTTGCACCTCTCTCAAAATTTGATGTAGTGCCACTTCCGCCAGGGGAAAGGCT	1200				
QY	1201	GGCCGCCACCAACCAACACACAGCAATGGCAACACCGCAGCAACCAATCAGATA	1260				
DB	1201	GGCCGCCACCAACCAACACACAGCAATGGCAACACCGCAGCAACCAATCAGATA	1260				
QY	1261	TATCAAAATGAATTAGAAGAACACACAGCCTCATGGACAGAAATTTGAGGGAGGGAAC	1320				
DB	1261	TATCAAAATGAATTAGAAGAACACACAGCCTCATGGACAGAAATTTGAGGGAGGGAAC	1320				
QY	1321	AAAGAAATCTTGGGGGGAAGAGTTTAAAGAAATTTGAAATTTGCTTGCAGATA	1380				
DB	1321	AAAGAAATCTTGGGGGGAAGAGTTTAAAGAAATTTGAAATTTGCTTGCAGATA	1380				
QY	1381	TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGGAAGAACACAGCACCCGGCTTGA	1440				
DB	1381	TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGGAAGAACACAGCACCCGGCTTGA	1440				
QY	1441	CCCACTGCAAGTGCATCGTGAACCTCTTTTGGTGCCAGTGTGGCAAGGCTCAGCCTC	1500				
DB	1441	CCCACTGCAAGTGCATCGTGAACCTCTTTTGGTGCCAGTGTGGCAAGGCTCAGCCTC	1500				
QY	1501	TCTGCCACAGAGTGGCCCCAGCTGGCAACATTTCTGGAGTGGCCATCCCAATTTCAATCA	1560				
DB	1501	TCTGCCACAGAGTGGCCCCAGCTGGCAACATTTCTGGAGTGGCCATCCCAATTTCAATCA	1560				
QY	1561	GTCCATAGAGCAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGGCTTGGGCTTTG	1620				
DB	1561	GTCCATAGAGCAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGGCTTGGGCTTTG	1620				
QY	1621	GTAGACTGTGCCACCAAGCGGTGTGTGTGAACGTGAAATTAAGAGCAAAAAA	1679				
DB	1621	GTAGACTGTGCCACCAAGCGGTGTGTGTGAACGTGAAATTAAGAGCAAAAAA	1679				

RESULT 7.
 US-09-978-585A-522
 : Sequence 522, Application US/05978585A
 : Publication No. US20030049633A1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi
 : APPLICANT: Baker Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Kijavins, Ivar J.
 : APPLICANT: Kuo, Sophia S.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Shelton, David L.
 : APPLICANT: Stewart, Timothy A.

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Oy 181 CTTTACGGGGTGGCTGCTCTGTCTCTTCCAGGAGTGCCCGTGCAGCGGAGATGC 240
Db 181 CTTTACGGGGTGGCTGCTCTGTCTCTTCCAGGAGTGCCCGTGCAGCGGAGATGC 240
Oy 241 CACCTTCCCAAGAGCTATGGACAACGTCAGCGGTCCGCGAGGGGGAGAGCGCACCTCTAG 300
Db 241 CACCTTCCCAAGAGCTATGGACAACGTCAGCGGTCCGCGAGGGGGAGAGCGCACCTCTAG 300
Oy 301 GTGCACTATTGACAACCGGTTCACCCGGGTGGCTGGCTGCTTAAACCCGACACCATCTCTA 360
Db 301 GTGCACTATTGACAACCGGTTCACCCGGGTGGCTGGCTGCTTAAACCCGACACCATCTCTA 360
Oy 361 TGCTGGGAATGACAAGTGTGCTTGGATCTTCGCGGTGCTCTTCTGACACACCCCAAC 420
Db 361 TGCTGGGAATGACAAGTGTGCTTGGATCTTCGCGGTGCTCTTCTGACACACCCCAAC 420
Oy 421 GCAGTACAGCATCGAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
Db 421 GCAGTACAGCATCGAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
Oy 481 GTGCGACAGACCAACCCCAAGACCTCTAGGTCGACCTCTTCTGACACACCCCAAC 540
Db 481 GTGCGACAGACCAACCCCAAGACCTCTAGGTCGACCTCTTCTGACACACCCCAAC 540
Oy 541 CAAATTTGTAGAGATTTCTCAGATATCTCCATATGAAAGGGAACATATATAGCTCTAC 600
Db 541 CAAATTTGTAGAGATTTCTCAGATATCTCCATATGAAAGGGAACATATATAGCTCTAC 600
Oy 601 CTGATAGCACTGTGTAGACAGAGCTTACGTTACTTGGAGACACATCTCTCCCAAGC 660
Db 601 CTGATAGCACTGTGTAGACAGAGCTTACGTTACTTGGAGACACATCTCTCCCAAGC 660
Oy 661 GTTGGGCTTTGTAGTGAAGCAATCTTGAATTTAGGCAATCAGGCGATCAGCGGAGCGTC 720
Db 661 GTTGGGCTTTGTAGTGAAGCAATCTTGAATTTAGGCAATCAGGCGATCAGCGGAGCGTC 720
Oy 721 AGGGGACTAGAGTGCAGTGCCTCCATATGAGTGGCGGCGCCCTGTTGACGAGAGTAAA 780
Db 721 AGGGGACTAGAGTGCAGTGCCTCCATATGAGTGGCGGCGCCCTGTTGACGAGAGTAAA 780
Oy 781 GGTCACTGTGAATCTATCCACCATATCTTCAAGAGCAAGGGTACAGTGTCCCGTGGG 840
Db 781 GGTCACTGTGAATCTATCCACCATATCTTCAAGAGCAAGGGTACAGTGTCCCGTGGG 840
Oy 841 ACAAAGGGGACACTGCTAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGA 900
Db 841 ACAAAGGGGACACTGCTAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGA 900
Oy 901 CAAGGATGACAAAGACTGATTGAGGAGAAAGGGGTGAAGTGAAGACAGACCTTT 960
Db 901 CAAGGATGACAAAGACTGATTGAGGAGAAAGGGGTGAAGTGAAGACAGACCTTT 960
Oy 961 CTTCTCAAACTCACTTCTCATATGCTCTGAAATGATGATGAGGACATGAGTGTGCT 1020
Db 961 CTTCTCAAACTCACTTCTCATATGCTCTGAAATGATGATGAGGACATGAGTGTGCT 1020
Oy 1021 GGCCTCAACAGCTGGGCGACCAATGCCAGCATCATGCTATTGTTGGTCCAGGCGCGCT 1080
Db 1021 GGCCTCAACAGCTGGGCGACCAATGCCAGCATCATGCTATTGTTGGTCCAGGCGCGCT 1080
Oy 1081 CAGCGAGGTGAGCAACGGCAGCTGAGGAGGCGAGGCTGCTGCTGCTGCTCTTCT 1140
Db 1081 CAGCGAGGTGAGCAACGGCAGCTGAGGAGGCGAGGCTGCTGCTGCTGCTCTTCT 1140
Oy 1141 GGTCTTGCACCTGCTCTCAAAATTTGATGTAGTGCCACTTCCCAACCGGAAAGGCT 1200
Db 1141 GGTCTTGCACCTGCTCTCAAAATTTGATGTAGTGCCACTTCCCAACCGGAAAGGCT 1200
Oy 1201 GCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
Db 1201 GCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
Oy 1261 TATACAAATGAATTTAGAGAAACACAGCTCTATGGGACAGAAATTTGAGGGAGGGGAAAC 1320

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RESULT 6

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US-09-978-608A-522
; Sequence 522, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fillvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978, 608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-522

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Db 1261 TATACAAATGAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
Oy 1321 AAGAATACCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAAAATTCCTTTCAGATA 1380
Db 1321 AAGAATACCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAAAATTCCTTTCAGATA 1380
Oy 1381 TTTAGTACAAATGGAGTTTCTTTTCCCAACGCGGAACACACACACCCGCGCTTGA 1440
Db 1381 TTTAGTACAAATGGAGTTTCTTTTCCCAACGCGGAACACACACACCCGCGCTTGA 1440
Oy 1441 CCCACTGCAAGCTGCATCTGCAACCTCTTTGGTCCAGTGTGGGCAAGGCTCAGCCCTC 1500
Db 1441 CCCACTGCAAGCTGCATCTGCAACCTCTTTGGTCCAGTGTGGGCAAGGCTCAGCCCTC 1500
Oy 1501 TCTGCCCCAGAGTGTGCCCCCAGCTGGAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Db 1501 TCTGCCCCAGAGTGTGCCCCCAGCTGGAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Oy 1561 GTCCATAGAGAGCAACAGATGAGACCTTCCCGGCCAAAGCTGCGCTGCGGGCCTTTTG 1620
Db 1561 GTCCATAGAGAGCAACAGATGAGACCTTCCCGGCCAAAGCTGCGCTGCGGGCCTTTTG 1620
Oy 1621 GTAGCTGTGCCACACAGCGCTGTGTGTGAACCTGAAATTAATAAGAGCAAAAAA 1679
Db 1621 GTAGCTGTGCCACACAGCGCTGTGTGTGAACCTGAAATTAATAAGAGCAAAAAA 1679

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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match
Best Local Similarity: 100.0%; Score 1679; DB 11; Length 1679;
Matches: 1679; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 1 GTTGTGCTCTTCACGAAACAGTGGATTAAATCTCTTCACAAGCTTGAGAGCAAC 60
|||||
DB 1 GTTGTGCTCTTCACGAAACAGTGGATTAAATCTCTTCACAAGCTTGAGAGCAAC 60
QY 61 AATCTATCAGGAAAGAAAGAAACCGAACTTGACAAAAAGAAAGAAAG 120
|||||
DB 61 AATCTATCAGGAAAGAAAGAAACCGAACTTGACAAAAAGAAAGAAAG 120
QY 121 AGAAAAAATCATGAAACCATCCAGCCAAAAATGCACAAATCTCTTGGCAAT 180
|||||
DB 121 AGAAAAAATCATGAAACCATCCAGCCAAAAATGCACAAATCTCTTGGCAAT 180

[illegible]

;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKTIQPKMNSISWAIETGLAALCLFQGVVPRSGDATEPKAMDNDVTVROGESATLRCTID	60
DB	1	MKTIQPKMNSISWAIETGLAALCLFQGVVPRSGDATEPKAMDNDVTVROGESATLRCTID	60
QY	61	NRVTRVAMLRNSTILYAGNDKWCLDPRVLLSNTOTQYSIEIQNDVDYDEGPTCSVQTD	120
DB	61	NRVTRVAMLRNSTILYAGNDKWCLDPRVLLSNTOTQYSIEIQNDVDYDEGPTCSVQTD	120
QY	121	NHFKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFV	180
DB	121	NHFKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFV	180
QY	181	SEDEYLEIOTIGTREGSDGYECSASNDVAPVVRVVKVTVNPPYISEAKGTGVPVQKGT	240
DB	181	SEDEYLEIOTIGTREGSDGYECSASNDVAPVVRVVKVTVNPPYISEAKGTGVPVQKGT	240
QY	241	LOCESAVPSAFOWYKDKKLEGGKVKVENRFFLSKLFFNVSEHDYGNVTCVASNK	300
DB	241	LOCESAVPSAFOWYKDKKLEGGKVKVENRFFLSKLFFNVSEHDYGNVTCVASNK	300
QY	301	LGHNTASIMLFGPGAVSEVNGTSRAGCVWLLPLLVLLHLLKF	344
DB	301	LGHNTASIMLFGPGAVSEVNGTSRAGCVWLLPLLVLLHLLKF	344

RESULT 9

US-09-978-403A-523
Sequence 523, Application US/09978403A
Publication No. US20030050240A1

GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavoin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey

;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C17
;; CURRENT APPLICATION NUMBER: US/09/978,403A
;; CURRENT FILING DATE: 2002-03-19
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
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 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07

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 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match: 100.0%; Score 1806; DB 11; Length 344;
 Best Local Similarity: 100.0%; Pred. No. 1.7e-150; Indels 0; Gaps 0;
 Matches 344; Conservative 0; Mismatches 0

QY	1	MKTIOPKHNSISWAIETGLAALCLFQGVVPSRSDATFPKAMDNVTVRGSATLRCTID	60
DB	1	MKTIOPKHNSISWAIETGLAALCLFQGVVPSRSDATFPKAMDNVTVRGSATLRCTID	60
QY	61	NRVTRVAMLNSTILYAGNDKWCCLDPVRLVLSNTQYISIEIONVDVYDEGYTCSVOTD	120
DB	61	NRVTRVAMLNSTILYAGNDKWCCLDPVRLVLSNTQYISIEIONVDVYDEGYTCSVOTD	120
QY	121	NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTICATGRPEPTVTVRHHISPKRAGFV	180
DB	121	NHPKTSRVHLIVQSPKIVEISSDISINEGNNISLTICATGRPEPTVTVRHHISPKRAGFV	180
QY	181	SEDEXLEIQGITREQSGDYECSSANDVAAPVVRVVKVTVNYPYIIEAKGTGVPVQKGT	240
DB	181	SEDEXLEIQGITREQSGDYECSSANDVAAPVVRVVKVTVNYPYIIEAKGTGVPVQKGT	240
QY	241	LOCEASAVPSAEFQWKDKRLTEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK	300
DB	241	LOCEASAVPSAEFQWKDKRLTEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK	300
QY	301	LIGHTNASIMLFGPGAVSEVSNGTSSRACVWLLPLLVHLLKAF	344
DB	301	LIGHTNASIMLFGPGAVSEVSNGTSSRACVWLLPLLVHLLKAF	344

RESULT 10
 US-09-978-564A-523
 ; Sequence 523, Application US/09978564A
 ; Publication No. US20030050241A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC25
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: US/09/978,564A
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 60/083742
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PRIOR APPLICATION NUMBER: 60/084366
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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 1806 DB 11 Length 344
 Best Local Similarity 100.0% Pred. No. 1.7e-150 Indels 0 Gaps 0
 Matches 344 Conservative 0 Mismatches 0
 QY 1 MKTIQPKMNSISWAIFTGLAALCLFQGVPRSGDATPFKAMDNTVVRQGESATLRCITID 60
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 DB 61 NRTRVAVLNRSITILYAGNDKWCCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTD 120
 QY 121 NHPKTSRVLHVQVSPKIVEISSDINSIGNNISLTCTATGRPEPTVTRHISPRKAVGFV 180
 DB 121 NHPKTSRVLHVQVSPKIVEISSDINSIGNNISLTCTATGRPEPTVTRHISPRKAVGFV 180
 QY 181 SEDEYLEIOGITREQSGDYECASNDVAAPVVRKVTNNYPPYISEAKGTGVPVQKGT 240
 DB 181 SEDEYLEIOGITREQSGDYECASNDVAAPVVRKVTNNYPPYISEAKGTGVPVQKGT 240
 QY 241 LOCEASAVPSAEFQYKDKRLIEGKGVKVENRPFLLSKLIFFNVSEHDYGNVTCVSNK 300
 DB 241 LOCEASAVPSAEFQYKDKRLIEGKGVKVENRPFLLSKLIFFNVSEHDYGNVTCVSNK 300
 QY 301 LGHTNASIMLFCPGAVSEVSNGTSSRAGCVWLLPLLVHLLKKF 344
 DB 301 LGHTNASIMLFCPGAVSEVSNGTSSRAGCVWLLPLLVHLLKKF 344

RESULT 11
 US-09-999-833a-523
 Sequence 523, Application US/09999833a
 Publication No. US20030054405A1
 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
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 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
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 APPLICANT: Hillan, Kenneth J.
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 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C65
 CURRENT APPLICATION NUMBER: US/09/999,833A
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: 05/918595
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTIQPKMHNISWAIFTGLAALCLFQGVPRSGDATEPKAMDNVTVRQGESATLRCTID 60
Db 1 MKTIQPKMHNISWAIFTGLAALCLFQGVPRSGDATEPKAMDNVTVRQGESATLRCTID 60
QY 61 NRVTAVLNRSTILYAGNDKWCCLDPVLLSNTQTQYSIEIQNVVDVDEGPTCSVQTD 120
Db 61 NRVTAVLNRSTILYAGNDKWCCLDPVLLSNTQTQYSIEIQNVVDVDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVESSDISINEGNNISLTCATGRPPTVTRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVESSDISINEGNNISLTCATGRPPTVTRHISPKAVGFV 180
QY 181 SEDYLEIOGITREQSGDYECASNDVAVPVVRKVTVNVPYVISEAKTGVPCOKGT 240
Db 181 SEDYLEIOGITREQSGDYECASNDVAVPVVRKVTVNVPYVISEAKTGVPCOKGT 240
QY 241 LOCEASVPSAEFQWKDKRLIEGKKGKGVKVENRPFSLKLIFFNVSDHGYNTVCVASK 300

Db 241 LQCEASAVPSAEFWYKDDRLTEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVSNK 300
QY 301 LGHTNASIMLFGAGVSEVSGTSSRAGCVWLLPLLVHLLKLF 344
Db 301 LGHTNASIMLFGAGVSEVSGTSSRAGCVWLLPLLVHLLKLF 344

RESULT 12
US-09-981-915A-523
Sequence 523, Application us/09981915A
Publication No. US20030054986A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
FILE OF INVENTION: AC18s Encoding the Same
FILE REFERENCE: P2630P1C12
CURRENT APPLICATION NUMBER: US/09/981,915A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
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 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MXTIOPKHNISWAIETGLAALCLFQGVPRSGDATFPKAMDNVTVRQGSATLRCTID 60

QY 61 NRTRVAVLNRSITLYAGNDKWCCLDPVLLSNTQTOYSIEIQNVDDVDEGPTCSVQTD 120
 DB 61 NRTRVAVLNRSITLYAGNDKWCCLDPVLLSNTQTOYSIEIQNVDDVDEGPTCSVQTD 120
 QY 121 NPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGPRPTVTRHISPKAVGFV 180
 DB 121 NPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGPRPTVTRHISPKAVGFV 180
 QY 181 SEDEYLTICITREQSGDYECASNDVAAPVVRVKVTVVTPPYPISEAKGTGVPVQCKT 240
 DB 181 SEDEYLTICITREQSGDYECASNDVAAPVVRVKVTVVTPPYPISEAKGTGVPVQCKT 240
 QY 241 LQCEASAVPSAEFQWKDDKRLIEGKGVKVENRPLSKLIFFFNVSEHDYGNITCVASNK 300
 DB 241 LQCEASAVPSAEFQWKDDKRLIEGKGVKVENRPLSKLIFFFNVSEHDYGNITCVASNK 300
 QY 301 LGHTNASIMLFGPGAVSEVSGTSTRRAGCVWLLPLLVLLHLKLF 344
 DB 301 LGHTNASIMLFGPGAVSEVSGTSTRRAGCVWLLPLLVLLHLKLF 344

RESULT 13
 US-09-978-824-523
 ; Sequence 523, Application US/09978824
 ; Publication No. US20030055216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Olang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC14
 ; CURRENT APPLICATION NUMBER: US/09/978,824
 ; CURRENT FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
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 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077641

[illegible]

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. NO. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKTIQPKHNSISNAIFTGLAALCLFQGVPRVRSNGDATFPKAMDNVTVROGESATLRCTID 60
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Db 61 NRVTRVAMLNSTILYAGNDKWCCLDPVVLLSNTOTQYSEIQNVDDYDEGPTCSVQTD 120
Oy 121 NHPKTSRHLIVQSPKIVEISSDINSINEGNNISLCTIATGREPTVTVRHISPKANGFV 180
Db 121 NHPKTSRHLIVQSPKIVEISSDINSINEGNNISLCTIATGREPTVTVRHISPKANGFV 180
Oy 181 SEDEVLETOGTRQSGDYECSSANDVAAPVVRVYKVTYKVPYISEAKGTGVPVQKGT 240
Db 181 SEDEVLETOGTRQSGDYECSSANDVAAPVVRVYKVTYKVPYISEAKGTGVPVQKGT 240
Oy 241 LCEASAVPSAEFOWYKDDKRLIEGKGVKVENRPFSLKIFFNVSEHDYGNVTCVASNK 300
Db 241 LCEASAVPSAEFOWYKDDKRLIEGKGVKVENRPFSLKIFFNVSEHDYGNVTCVASNK 300
Oy 301 LGHTNASIMLFGPGAVSEVSGNSTRAGCWWLLPLLVHLHLKPF 344
Db 301 LGHTNASIMLFGPGAVSEVSGNSTRAGCWWLLPLLVHLHLKPF 344

RESULT 14
US-09-918-585A-523
; Sequence 523, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottschalk, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paonl, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C21
CURRENT APPLICATION NUMBER: US/09/9778,423A
CURRENT FILING DATE: 2002-05-16
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1806; DB 11; Length 344;
Best-Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MKTIOPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVROGESATLRCTID 60
Db 1 MKTIOPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVROGESATLRCTID 60

Oy 61 NRVTVMALNRSTILYAGNDKWCIDPRVLLSNTOYTSIEIONVDVDEGPTCSVQTD 120
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Search completed: September 11, 2003, 03:07:32
Job time : 53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2003, 03:06:34 : Search time 4576 Seconds
(without alignments)
3075.374 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 1806

Sequence: 1 MKTIQPKMINSISWAFITGL.....RRAGCVLLPLVLLHLLKF 344

Scoring table: BLOSUM62.

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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: DEV=xl

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41: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1806	100.0	1679	6	AX358872 Sequence
2	1806	100.0	1679	6	AX362365 Sequence
3	1806	100.0	1679	6	AX403748 Sequence
4	1806	100.0	1679	6	AX454470 Sequence
5	1806	100.0	1679	6	AX464242 Sequence
6	1806	100.0	1679	6	AX490948 Sequence
7	1655.5	92.2	1839	6	AX655342 Sequence
8	1655.5	92.2	1839	9	AF126426 Homo sapi
9	1650	91.4	1068	6	AX655344 Sequence
10	1647.5	91.2	1615	10	BC023307 Mus muscu
11	1644	91.0	1104	6	AX655346 Sequence
12	1639.5	90.8	2040	10	RN016845 UI6845 Rattus norv
13	1638	90.7	1140	6	AX655348 Sequence
14	1616.5	89.5	1410	10	AF282980 Mus muscu
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16	1477.5	81.8	1257	5	GCCEP11 272497 G.gallus mr
17	1428	79.1	1058	5	AF292935 Gallus ga
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ALIGNMENTS

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LOCUS AX358872 1679 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 125 from Patent WO0193983.
ACCESSION AX358872
VERSION AX358872.1 GI:18675337
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 125 13-DEC-2001;
Genentech Inc. (US)
FEATURES
source
Location/Qualifiers
1. 1679
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 498 a 432 c 419 g 330 t
ORIGIN
Alignment Scores:
Pred. No.: 6,67e-158 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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LOCUS AX362365 1679 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 125 from Patent WO0208288.
ACCESSION AX362365
VERSION AX362365.1 GI:18694640
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 125 31-JAN-2002;
Genentech, Inc (US)
FEATURES
source
Location/Qualifiers
1. 1679
/organism="Homo sapiens"
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BASE COUNT 498 a 432 c 419 g 330 t
ORIGIN
Alignment Scores:
Pred. No.: 6,67e-158 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-017-084A-523 (1-344) x AX362365 (1-1679)
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LOCUS AX403748 1679 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 103 from Patent WO0077037.
ACCESSION AX403748
VERSION AX403748.1 GI:21437184
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi, A., Baker, K., Botstein, D., Desnoyers, L., Eaton, D.L.,
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P., Gurney, A., Kijavini, I.J., Mather, J.,
Napier, J., Pan, J., Paoni, N., Roy, M., Tamas, D., Watanabe, C.,
Williams, P.M., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;
Genentech Inc. (US)
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Location/Qualifiers
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/mol_type="genomic DNA"
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BASE COUNT 498 a 432 c 419 g 330 t
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Score: 1806.00 Matches: 344
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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 DB 1154 CTCTCAAAATTT 1165

RESULT 4
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 LOCUS
 DEFINITION Sequence 55 from Patent WO0208284.
 ACCESSION AX454470
 VERSION AX454470.1 GI:21713859
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1
 Baker.K.P., Ferrara.N., Gerber.H., Gerritsen.M.E., Goddard.A.,
 Godowski.P.J., Gurney.A.L., Hillan.K.J., Marsters.S.A., Pan.J.,
 Paoni.N.F., Stephan.J.P., Watanabe.C.K., Williams.P.M., Wood.W.I.
 and Ye.W.
 TITLE Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis
 JOURNAL Patent: WO 0208284-A 55 31-JAN-2002;
 Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
 (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
 Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
 Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US);
 Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
 Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
 I. (US)

FEATURES
 Location/Qualifiers
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BASE COUNT 498 a 432 c 419 g 330 t

ORIGIN

Alignment Scores: 6.67e-158 Length: 1679

Pred. No.: 1806.00 Matches: 344

Score:

Percent similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 DB 374 AAGTGTGCTGGATCCCTCGGTGGTCTCTTCTGAGCAACACCAACGAGTACAGCATC 433
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 QY 121 AsnHisProLysThrSerArgValHisLeuLeuValGlnValSerProLysIleValGlu 140
 DB 494 AACCCCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTCAGATATCTCCATTAATGAAGGGAACATATATAGCTCACCCTCATAGCACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGCCCTACCGTGTACCTTGAGACACATCTCTCCCAAGGGTGTGCTTGTG 673
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 DB 674 AGTGAAGACCAATACCTTGAATTCAGGCGATCACCGGGAGCAGTCAGGGAGTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValAlaArgValValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCCCAATGACGTGGCGCGCGGTGACGAGAGTAAAGGTACCGGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTTCAGAGGCCAGGGGTACAGGTGTCCTCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLysAspAspLys 260
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 QY 261 ArgLeuIleGluGlyLysGlyValValValValValValValValValValValValVal 280
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 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
 DB 1094 AACGGCAGCTGAGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1153

QY 291 GlyAsnThrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
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 QY 311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
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 DB 1255 TGCTGCTGCTCTCTGGTCTTGCACCTGCTTCTCAAAATTT 1296

RESULT 9
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 DEFINITION AX65344
 VERSION AX65344.1 GI:29290465
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 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Sellar, G.C. and Gabra, H.
 TITLE Cancer
 JOURNAL Patent: WO 03002765-A 102 09-JAN-2003;
 Cancer Research Technology Limited (GB)
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 Best Local Similarity: 93.33% Mismatches: 8
 Query Match: 91.36% Indels: 13
 DB: 6 Gaps: 2

US-10-017-084A-523 (1-344) x AX65344 (1-1068)

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 QY 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
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 QY 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
 DB 151 GAGAGCCGCCCTCAGGTGCATATTGACACCGGCTACCGGGTGGCTGGCTGCTTAAC 210
 QY 71 ArgSerThrIleLeuThrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
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 QY 191 IleThrArgGlnSerGlyAspThrGlyCysSerAlaSerAsnAspValAlaAlaPro 210
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 LOCUS Mus musculus neurotrophin, mRNA (cdna clone MGC:30504
 DEFINITION IMAGE:4480983), complete cds.
 ACCESSION BC023307
 VERSION BC023307.1 GI:23958300
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 1615)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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 Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,
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 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,


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Db 511 CACATCTCTCCAAAGGGTGGCTTTGCTGAGTGAAGCAATACCTTGGAAATTCAGGGC 570
Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerIleAsnAspValAlaAlaPro 210
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Qy 231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
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Qy 316 ValSerGluValSerAsnGlyThrSerArgAlaGlyCysValrPrLeuLeuProLeu 335
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Db 1111 CTGGTCTTGCACCTGCTCTCAAAATTT 1137

RESULT 14
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LOCUS AF282980 1410 bp mRNA linear ROD 01-FEB-2001
DEFINITION Mus musculus neurotrophin mRNA, complete cds.
ACCESSION AF282980
VERSION AF282980.1 GI:12642539
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
Mus.
1 (bases 1 to 1410)
Kim, T.H., Choi, S.C., Kim, J., Jeon, J.W., Kim, K.D. and Lee, S.H.
Cloning and expression of mouse neurotrophin gene in the developing
nervous system
Unpublished
JOURNAL
2 (bases 1 to 1410)
Kim, T.H., Choi, S.C., Kim, J., Jeon, J.W., Kim, K.D. and Lee, S.H.
Direct Submission
AUTHORS
TITLE Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea
JOURNAL University, 1,5-ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea
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 VERSION BC050716.1 GI:30047134
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 SOURCE Homo sapiens (human)
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE 1 (bases 1 to 1325)
 AUTHORS Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
 Altchul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouford, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL 22388257
 MEDLINE 12477932
 PUBMED
 REFERENCE 2 (bases 1 to 1325)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 CONTACT NIH-MGC Project URL: http://mgc.nci.nih.gov
 CONTACT: MGC help desk
 EMAIL: cgabp3-r@mail.nih.gov
 TISSUE Tissue Procurement: ATCC/DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: http://www-shgc.stanford.edu
 Contact: (Dickson, Mark) mcdpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov
 Series: IRAK Plate: 110 Row: m Column: 8
 This clone was selected for full length sequencing because it
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US-10-017-084A-523 (1-344) x BC050716 (1-1325)

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GenCore version 5.1.6
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Listing first 45 summaries

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-O/cg2.1/USPRO_spool_PUS10017084/runat_09092003_141325_21860/app.query.fasta_1.519
-DB-N_Geneseq_19Jun03 -QMT-fastap -SUFFIX-p2n.rng -MINMATCH-0.1 -LOOPEL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cd1
-LIST-45 -DOALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US10017084 -CGN_1_1_190 -runat_09092003_141325_21860 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEOQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOF-6
-FGAPEXT-7 -YGAPOF-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1806	100.0	1032	21	AAZ47892 Human protein enco
2	1806	100.0	1679	20	AAZ34324 Human PRO337 nucle
3	1806	100.0	1679	21	AAC78590 Human PRO337 nucle
4	1806	100.0	1679	22	AAS21431 Human cDNA sequenc
5	1806	100.0	1679	22	AAC87037 Nucleotide sequenc
6	1806	100.0	1679	24	ABL95588 Human anglogenesis
7	1806	100.0	1679	24	ABL88099 Human PRO337 cDNA
8	1806	100.0	1679	24	ABK33598 cDNA encoding huma
9	1806	100.0	1679	25	ACA60526 Novel human secret
10	1806	100.0	1679	25	ACA03790 cDNA encoding huma
11	1806	100.0	1679	25	ACA04211 Human cDNA encodin
12	1806	100.0	1679	25	ACA04516 Novel human secret
13	1806	100.0	1679	25	ACA04996 Novel human secret
14	1806	100.0	1679	25	ABX89328 DNA encoding novel
15	1806	100.0	1679	25	ABX92696 cDNA encoding huma
16	1806	100.0	1693	21	AAZ47893 Human protein enco
17	1799	99.6	1603	21	AAZ88790 Human SECX cDNA C1
18	1799	99.6	1603	21	AAZ88791 Human SECX cDNA C1
19	1756	97.2	1873	24	ABK4272 Human kruppel asso
20	1752	97.0	1890	22	AA159655 Human polynucleoti
21	1665.5	92.2	1878	22	AA157869 Lung cancer-associ
22	1665.5	92.2	1839	25	ABX76448 Human protein enco
23	1642	90.9	939	21	AAZ47894 Rat oploid recepto
24	1286.5	71.2	3069	14	AAQ51015 Rat oploid recepto
25	1260	69.8	2179	14	AAQ51017 Rat oploid recepto
26	1259	69.7	2337	14	AAQ51016 Human secreted exp
27	1173	65.0	1832	21	AAA44536 Human limbic syste
28	932.5	51.6	1411	24	AAZ50356 Human cDNA #560 d1
29	931.5	51.3	1195	25	ABX63560 Rat LAMP coding se
30	926.5	51.3	1014	17	AAT42081 Rat LAMP coding se
31	926.5	51.3	1238	17	AAT42080 Rat LAMP coding se
32	923.5	51.1	977	17	AAT42079 Human LAMP residue
33	913	50.6	1307	17	AAT42116 Rat LAMP clone 6c
34	908	50.3	924	17	AAT42084 Human LAMP residue
35	907	50.2	945	17	AAT42085 Rat LAMP residues
36	905	50.1	930	17	AAT42083 Rat mature LAMP co
37	902	49.9	912	17	AAT42082 Human mature LAMP co
38	893	49.4	1757	25	ABZ76264 Human GENSET cDNA
39	886.5	49.1	861	17	AAT42086 Rat LAMP residues
40	885.5	49.0	861	17	AAT42087 Human colon cancer
41	885	49.0	1153	22	AAH34425 Human EST DNA42301
42	859	47.6	503	20	AAZ34325 Human EST DNA42301
43	859	47.6	503	21	AAC78591 Human PRO337 EST p
44	859	47.6	503	25	ABX52697 Human NOV12a encod
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ALIGNMENTS

RESULT 1
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ID AAZ47892 standard; cDNA; 1032 BP.
XX
AC AAZ47892;
XX
DT 10-MAR-2000 (first entry)
XX
DE Human protein encoding cDNA SEQ ID NO:2.
XX
KW Human; haematopoietic cell regulation; tissue generation; repair;
KW activin; inhibitor; taxis; chemotaxis; blood coagulation; thrombus;
KW receptor; ligand; autoimmunity; infection-related immunodeficiency;
KW inflammatory disorder; neurological disease; ss.
XX
OS Homo sapiens.
XX


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PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 05-MAY-1998; 98US-0084414.
PR 05-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.

PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX (GETH ) GENENTECH INC.
XX
XX Wood WI, Goldard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI: 1999-551358/46;
XX P-PSDB; AA41773.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders
XX
XX Claim 2; Fig 221; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AA233891 to
XX AA234338, and AA41685 to AA41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
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XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:
Pred. No.: 8,55e-167 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

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Db 134 ATGAAMCCATCCAGCAAAATGCAATTCATCTCTTGGGCAATCTTCCGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Qy 41 AlaMetAspAsnValThrValArgGlnGlyLeuSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACACCGTGCAGCGTCCGGCAGGGGAGAGCCACCTCAGGTGACATTGAC 313
Qy 61 AsnArgValThrArgValAlaIlePleuAsnArgSerThrIleLeuThrAlaGlyAsnAsp 80
Db 314 AACCGGTGTCACCGGTGCTGGCTGCTAAACCGCAGCAGCATCTCTATGTTGGAAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnThrSerIle 100
Db 374 AAGTGGTGCTGCTGGATCCTCGCTGCTCTTCTGAGCAACCAACCAACCAACCAACCA 433
Qy 101 GluIleGlnAsnValAspValThrAspGluClyProThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACCGTGTGATGTATGACAGAGGGCCCTTACACCTGCTCGTGCACAGAC 493
Qy 121 AsnHisProLysThrSerArgValHisIleuIleValGlnValSerProLysIleValGlu 140
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 Db 554 ATTCTTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACCCTGCACTACT 613
 Qy 161 GlyArgProGluProThrValThrIleThrIleThrIleThrIleThrIleThrIleThr 180
 Db 614 GGTAGACAGAGCCTACGGTTACTTGGACACATCTCTCCCAAGCGGTGGCTTGTG 673
 Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 Db 674 AGTGAAGACGAATACTTGGAAATTCAGGCGCATCCCGGGAGCAGTCAGGGGACTAGG 733
 Qy 201 CysSerAlaSerAsnAspValAlaIleProValValArgValValValValValVal 220
 Db 734 TGCAGTGGCTCCATGACGTGGCGCGCGCGTGTGTACGGAGCTAAAGGTCACTGAA 793
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 Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspLys 260
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 Qy 261 ArgLeuIleGluGlyLysGlyValLysValGlnValGlnValGlnValGlnValGln 280
 Db 914 AGACTGATGAGGAAGAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973
 Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 Db 974 ATCTCTTCAATGCTCTGAACATGACTATGGGAACATACACTTTCGCTGGCCCTCC 1033
 Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCCACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGCTCAGCGAGGTGAGC 1093
 Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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 ID AAC78590 standard; cDNA: 1679 BP.
 AC AAC78590;
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 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO337 nucleotide sequence SEQ ID NO:522.
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 KW Human; secreted protein; transmembrane protein; PRO; EST; cytotstatic;
 XX expressed sequence tag; detection; cancer; ss.
 OS Homo sapiens.
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-2000; 2000WO-US11274.
 PR 06-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 (GETH) GENENTECH INC.
 XX
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI: 2000-611443/58.
 DR P-PSDB; ABA44329.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities.
 XX
 PS Claim 2; Fig 22; 63pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
 Alignment Scores:
 Pred. No.: 8,55e-167 Length: 1679
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-10-017-084A-523 (1-344) x AAC78590 (1-1679)
 Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAACCAATCCAGCAAAATGCAATTCATCTCTGGGCAATCTTCACGGGCTG 193
 Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTGTGTCTCTTCAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 253
 Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGGACAACCGTCGCTCGCGAGGGAGCGCCACCTCAGCTGCTATTGAC 313
 Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 Db 314 AACCGGCTCACCGGGTGGCTGGCTGCTAAACCGCAGCACCCTCTCTATGTGGGAATGAC 373
 Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 Db 374 AAGTGGTGGCTTGGATCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 433

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OY 101 GluIleGlnAsnValaspValtyrAspGluGlyProtyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGACGAGTGGATGTGTATGACGAGGGCCCTTACACCTCTCGTGCAGACAGAC 493
OY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGCTCCACCTCATGTGTGCAAGTATCTCCCAAAATGTAGAG 553
OY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAAAGGGAACATATTAGCTCCACCTGCATCAACT 613
OY 161 GlyArgProGluProThrValThrTPArgHisIleSerProLysAlaValAlaGlyPheVal 180
DB 614 GGTAGACAGAGCCTACGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTTGTG 673
OY 181 SerGluAspGluTyrLeuGluIleGlnGlnIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGAGAACTTGGAAATTCAGGCATCAGCCGGGAGCAGTCAGGGGACTACGAG 733
OY 201 CysSerAlaSerAsnAspValAlaIleProValValArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCAAATGACGTGGCGCGCCGCTGGTACGAGAGTAAAGTTCACCTGAAC 793
OY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTTTCAGAAAGCAAGGTTACAGGTGTCCCGCTGGGACAAAAGGGACA 853
OY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrIleLysAspLys 260
DB 854 CTCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCACAGTGTACAGGATGACAAA 913
OY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGAAAGAGGGGTGAAGTGAAGTGAAGAACAGCTTCTCTCAAACTC 973
OY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaAsnLys 300
DB 974 ATCTTCTCATGTCTCTGACATGACTATGGAACTACACTTGGCTGGCTCCAAACAG 1033
OY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGCCACCAATGACGATCATGTATTGTCCAGCGCCGTCACGAGGTGAGC 1093
OY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
DB 1094 AAGCGCAGCTCAGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
OY 341 LeuLeuLysPhe 344
DB 1154 CTCTCAAAATTT 1165
RESULT 4
AAS21431
ID AAS21431 standard; cDNA; 1679 BP.
AC AAS21431;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human cDNA sequence encoding for PRO337 polypeptide.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
NW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS Homo sapiens.
XX
XX WO200140466-A2.
XX
XX 07-JUN-2001.
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XX 01-DEC-2000; 2000WO-US32678.
PF 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30959.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US0027.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US15264.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Garritsen WE, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2001-408281/43.
XX P-PSDB: AAU12359.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
other PRO polypeptides, link bioactive molecules to cells expressing
PRO polypeptides, and detect the presence of mammalian tumours e.g.
lung, breast, prostate, cervical
XX
PS Claim 3; Fig 375; 813pp; English.
XX
XX AAS21244-AAS21518 encode for novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bioactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or
of T-lymphocytes, the release of a cytokine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
to factor VIIA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
PRO polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
Alignment Scores:
Pred. No.: 8,55e-167 Length: 1679
Score: 1806.00 Matches: 344
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PR	16-SEP-1998;	98W0-US193300
PR	17-SEP-1998;	98W0-US191437
PR	20-NOV-1998;	98W0-US24855
PR	25-NOV-1998;	98W0-US251108
PR	01-DEC-1998;	98W0-US25108
PR	08-MAR-1999;	98W0-US05028
PR	02-JUN-1999;	98W0-US12252
PR	01-SEP-1999;	98W0-US20111
PR	08-SEP-1999;	98W0-US20594
PR	15-SEP-1999;	98W0-US21090
PR	15-SEP-1999;	98W0-US21457
PR	30-NOV-1999;	98W0-US28313
PR	01-DEC-1999;	98W0-US28101
PR	02-DEC-1999;	98W0-US28565
PR	20-DEC-1999;	98W0-US30899
PR	05-JAN-2000;	2000W0-US00219
PR	18-FEB-2000;	2000W0-US04342
PR	18-FEB-2000;	2000W0-US04342
PR	22-FEB-2000;	2000W0-US04141
PR	01-MAR-2000;	2000W0-US05601
PR	02-MAR-2000;	2000W0-US05601
PR	09-MAR-2000;	2000W0-US06471
PR	20-MAR-2000;	2000W0-US07377
PR	30-MAR-2000;	2000W0-US08439
PR	15-MAY-2000;	2000W0-US13358
PR	17-MAY-2000;	2000W0-US13705
PR	22-MAY-2000;	2000W0-US14042
PR	30-MAY-2000;	2000W0-US14941
PR	02-JUN-2000;	2000W0-US15264
PR	11-AUG-2000;	2000W0-US22031
PR	23-AUG-2000;	2000W0-US23322
PR	24-AUG-2000;	2000W0-US23328
PR	01-DEC-2000;	2001W0-US32578
PR	28-FEB-2001;	2001W0-US06520
PR	30-MAY-2001;	2001W0-US17443
PR	01-JUN-2001;	2001W0-US17800
PR	20-JUN-2001;	2001W0-US19692
PR	29-JUL-2001;	2001W0-US21066
PR	09-AUG-2001;	2001W0-US21735
PR	26-AUG-1997;	97U0-US659749
PR	17-SEP-1997;	97U0-US591155
PR	18-SEP-1997;	97U0-US926339
PR	19-SEP-1997;	97U0-US959889
PR	17-OCT-1997;	97U0-US628585
PR	24-OCT-1997;	97U0-US628169
PR	24-OCT-1997;	97U0-US630829
PR	27-OCT-1997;	97U0-US633299
PR	29-OCT-1997;	97U0-US637339
PR	21-NOV-1997;	97U0-US663649
PR	25-NOV-1997;	97U0-US668409
PR	16-DEC-1997;	97U0-US695649
PR	09-FEB-1998;	98U0-US740869
PR	09-FEB-1998;	98U0-US740929
PR	25-MAR-1998;	98U0-US792949
PR	08-APR-1998;	98U0-US810439
PR	10-AUG-1998;	98U0-US859889
PR	18-AUG-1998;	98U0-US970009
PR	09-SEP-1998;	98U0-US960019
PR	10-SEP-1998;	98U0-US988119
PR	10-SEP-1998;	98U0-US988112
PR	17-SEP-1998;	98U0-US1008589
PR	24-SEP-1998;	98U0-US1019229
PR	28-OCT-1998;	98U0-US1060329
PR	20-NOV-1998;	98U0-US1093049
PR	23-MAR-1999;	99U0-US1257789
PR	15-JUN-1999;	99U0-US1366595
PR	26-JUL-1999;	99U0-US1450709
PR	20-AUG-1999;	99U0-US1456989
PR	07-DEC-1999;	99U0-US1493669
PR	15-NOV-2001;	2001U0-US002796
XX		

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Borstein DA, Deanovers L, Eaton DL,
 PI Parrara N, Fong S, Gao W, Garber H, Gerlitsen ME, Goddard A,
 PI Godowski PJ, Cliney AL, Kljavin IJ, Mather JP, Napier MA, Pan J,
 PI Poon NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
 PI Wood WI, Zhang Z;
 XX
 DR: 2003-328482/31.
 DR P-PSDB; AB072061.
 XX
 Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, for identifying agonists
 PT or antagonists of polypeptide, and as molecular weight markers
 XX
 PS Claim 2; Fig 51; 254pp; English.
 XX
 CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
 CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337,
 CC PRO1411, PRO10096, PRO246, PRO307, PRO6003, fibroblast growth factor
 CC receptor (FGFR)-3, FGFR-4, FGFR-2, PRO6004, PRO4356, PRO2630,
 CC PRO265 or PRO951 polypeptides, and for linking a bioactive molecule to a
 CC cell expressing the above polypeptides. The bioactive molecule, a toxin,
 CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
 CC identify other proteins or molecules involved in binding interaction.
 CC The polynucleotide (II) encoding (I) is useful in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, for generating
 CC transgenic animals or knockout animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, to
 CC construct hybridisation probes for mapping the gene which encodes the
 CC PRO and for the genetic analysis of individuals with genetic disorders,
 CC in gene therapy, for chromosome identification and as a chromosome
 CC marker. (I) and (II) are useful for tissue typing. This sequence
 CC encodes a novel human secreted and transmembrane PRO polypeptide.
 XX
 SO Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-017-084A-523 (1-344) x ACA60526 (1-1679)

Qy 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAACCAATCCAGCCAAATGACCAATTCATCTTGGGCAATCTTACGGGGCTG 193
 Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTCTGCTCTCTTCAAGAGTGCCTGGCGGAGAGATGACATCCACCTTCCCAAA 253
 Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGGACACAGTGCAGGTCCGGCAGGGGAGAGAGCCACCTCAGTGACATTGAC 313
 Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuThrAlaGlyAsnAsp 80
 Db 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
 Db 374 AAGTGGTGGTATCTCGCTGGCTGCTCTTCTGAGCAACACCAACAGCAGTACAGATC 433
 Qy 101 GluIleGlnAsnValAspValTrpAspGlyProThrCysSerValClnThrAsp 120
 Db 434 GAGATCCAGAGAGTGGTATGATACGAGGGCCCTTACACCTGCTGCGTGCACAGAC 493
 Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140

Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
 Qy 141 IleSerSerAspIleSerIleAsnGlnGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCCTGCATGACACT 613
 Qy 161 GlyArgProGlnProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GTAGACAGAGCTACGGTACTTGGAGACATCTCTCCCAAGCCGTGGCTTGTG 673
 Qy 181 SerGluAspGlyTrpLeuGlnIleGlnGlyIleThrArgGluGlnIleSerGlyAspTrpGlu 200
 Db 674 AGTGAAGCAATATCTTGAATTCAGGGGATCACCAGGAGCAGTCAAGGAGTACGAG 733
 Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValValAsn 220
 Db 734 TGCAGTCCCTCAATGACGTGGCCGCCCGCTGTACGGAGATTAAGGTACCGTGAAC 793
 Qy 221 TyrProProTyrIleSerGlnAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATACATTTTCAAGAGCCCAAGGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
 Qy 241 LeuGlnCysGlnAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 Db 854 CTGCAAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
 Qy 261 ArgLeuIleGlnGlyLysGlyValValValValValValValValValValValValVal 280
 Db 914 AGACTGATTCAAGAAAGAAAGGGGTGAAAGTGAAGGAAAGACAGACCTTTCTCTCAAAACTC 973
 Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTCAATCTCTCTGAACATGACTATGGGAACACTACACTTGGCTGGCTCCCAACAG 1033
 Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320
 Db 1034 CTGGGCCACACCAATGCCAGCATCTATTTGGTCCAGGCGCGTCAGGAGGTGAGC 1093
 Qy 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 Db 1094 AACGGCAGCTGAGAGGGGAGGCGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
 Qy 341 LeuLeuLysPhe 344
 Db 1154 CTCTCAAAATTT 1165

RESULT 10
 ACA03790
 ID ACA03790 standard; cDNA; 1679 BP.
 XX
 AC ACA03790;
 XX
 DT 23-MAY-2003 (first entry)
 XX
 DE cDNA encoding human PRO polypeptide #188.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder;
 KW cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003036180-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 09-MAY-2002; 2002US-0143114.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12436.
 PR 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US24855.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 98WO-US00106.
PR 08-MAR-1999; 98WO-US05028.
PR 10-MAR-1999; 98WO-US05190.
PR 20-APR-1999; 98WO-US08615.
PR 14-MAY-1999; 98WO-US10733.
PR 02-JUN-1999; 98WO-US12252.
PR 03-SEP-1999; 98WO-US20111.
PR 08-SEP-1999; 98WO-US20594.
PR 13-SEP-1999; 98WO-US21090.
PR 15-SEP-1999; 98WO-US21547.
PR 05-OCT-1999; 98WO-US23089.
PR 29-NOV-1999; 98WO-US28214.
PR 30-NOV-1999; 98WO-US28313.
PR 30-NOV-1999; 98WO-US28409.
PR 01-DEC-1999; 98WO-US28301.
PR 01-DEC-1999; 98WO-US28634.
PR 02-DEC-1999; 98WO-US28551.
PR 02-DEC-1999; 98WO-US28564.
PR 02-DEC-1999; 98WO-US28565.
PR 16-DEC-1999; 98WO-US30095.
PR 20-DEC-1999; 98WO-US30911.
PR 20-DEC-1999; 98WO-US30999.
PR 22-DEC-1999; 98WO-US30720.
PR 30-DEC-1999; 98WO-US31243.
PR 30-DEC-1999; 98WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 13-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23521.
PR 08-NOV-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06866.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 23-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0860216.
PR 10-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 13-DEC-2001; 2001US-0028072.
XX (GETH) GENENTECH INC.
XX Baker RP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332040/31;
XX P-PSDB; AB066757.
XX New secreted and transmembrane PRO nucleic acids, useful for gene
XX therapy, in chromosome and gene mapping, as chromosome markers, in
XX tissue typing, and in chromosome identification
XX Claim 2; Fig 375; 660pp; English.
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The
XX PRO polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides for
XX linking bioactive molecules to cells expressing PRO polypeptides,
XX for modulating biological activities of cells expressing PRO
XX polypeptides, and for identifying agonists or antagonists.
XX The PRO polypeptides are useful for stimulating the release of
XX the tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
XX proliferation or differentiation of chondrocytes, and detecting the
XX presence of tumours. The polynucleotide sequences encoding PRO
XX polypeptides are useful as hybridisation probes, in chromosome and
XX gene mapping, in the generation of antisense RNA and DNA, in the
XX preparation of PRO polypeptides, for generating transgenic animals or
XX knockout animals, for the genetic analysis of individuals with genetic
XX disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
XX encoding the human PRO polypeptides of the invention.
XX Note: The sequence data for this patent was obtained in electronic
XX format directly from the USPTO web site at
XX seqdata.uspto.gov/psipsdIdentEntry.html.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
Alignment Scores:
Pred. No.: 8,55e-167 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0
US-10-017-084A-523 (1-344) x ACA03790 (1-1679)
Qy 1 MetLysThrIleClnProLysMethIsAsnSerIleSerrTrpAlaIlePheThrGlyLeu 20

Db 134 ATGAAACCATCCAGGCAAAATGCAAAATCTATCTCTTGGCAATCTTCCAGGGGCTG 193
Oy 21 AlaAlaLeucysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCTGGCGAGCGAGATGCCACCTTCCCAAA 253
Oy 41 AlameAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAACGTGACGCTCCGGCAGGGGAGAGCCACCTCAGGTGCACATATGAC 313
Oy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGCCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
Oy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrSerIle 100
Db 374 AAGTGGTGGCTGGATCTCGCGTGGTCTTCTGAGCAACACCAACGACGATCAGCATC 433
Oy 101 GluIleGlnAsnValAspValTyArgValHisIleValGlnValSerProLysIleValGlu 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCACACAGAC 493
Oy 121 AsnHisProLysThrSerArgValHisIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGTGCCACCTCATGTGCAAGTATCTCCCAAAATGTAGAG 553
Oy 141 IleSerSerAspIleSerIleAsnGlnGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTACCTGCATGACAACT 613
Oy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACAGAGCCTACGCTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
Oy 181 SerGluAspGluTyLeuGluIleGlnGlyIleThrArgGlnGlnSerGlyAspTyThrGlu 200
Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGGCATCACCGGGGAGCAGTACGGGACTAGCAG 733
Oy 201 CysSerAlaSerAsnAspValAlaLaProValValArgValLysValThrValAsn 220
Db 734 TGCAGTGCCTCAATGACGTGGCGCGCGCTGGTACGGAGAGTAAGGTACCGTGAAC 793
Oy 221 TyrProTyIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTCAGAACCCAGGGTACAGTGTCCCGCTGGGACAAAGGGGACAA 853
Oy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyIleAspAspLys 260
Db 854 CTGCACTGTGAGCCCTCAGCAGTCCCTCAGCAGANTTCCAGTGGTACAAAGATGACAAA 913
Oy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTTGAAGAAAGAAAGGTGAAGTGAAGAAACAGACCTTCTCTCAAAACTC 973
Oy 281 IlePhePheAsnValSerGluHisAspTyArgLysAsnTyThrCysValAlaSerAsnLys 300
Db 974 ATCTCTTCAATGCTCTGAACATGACTATGGAACTACACTTGGCGTGGCTCCCAACAAAG 1033
Oy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGCTCAGGAGGTGAGC 1093
Oy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGCGACGTCGAGGAGGCGAGCTGCTGCTGGCTGCTCTTCTGCTCTTGCACCTG 1153
Oy 341 LeuLeuLysPhe 344
Db 1154 CTCTCAAAATTT 1165

RESULT:11
ACA04211

ID XX ACA04211 standard; cDNA; 1679 BP.
AC XX ACA04211;
DT XX 27-MAY-2003 (first entry)
XX XX Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
DE XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW KW Inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW KW Infertility; birth defects; premature aging; AIDS; biosensor;
KW KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW KW bioeffector; tumour.
XX XX Homo sapiens.
OS XX Homo sapiens.
PN XX US2003032155-A1.
XX XX 13-FEB-2003.
PD XX 03-MAY-2002; 2002US-0137865.
XX XX 31-MAR-1997; 97WO-US05230.
PR PR 12-JUN-1998; 98WO-US12456.
PR PR 14-JUL-1998; 98WO-US14352.
PR PR 28-AUG-1998; 98WO-US17888.
PR PR 10-SEP-1998; 98WO-US18824.
PR PR 14-SEP-1998; 98WO-US19093.
PR PR 14-SEP-1998; 98WO-US19094.
PR PR 14-SEP-1998; 98WO-US19177.
PR PR 16-SEP-1998; 98WO-US19330.
PR PR 17-SEP-1998; 98WO-US19437.
PR PR 07-OCT-1998; 98WO-US21141.
PR PR 29-OCT-1998; 98WO-US22991.
PR PR 20-NOV-1998; 98WO-US24855.
PR PR 01-DEC-1998; 98WO-US25108.
PR PR 05-JAN-1999; 99WO-US00106.
PR PR 08-MAR-1999; 99WO-US05028.
PR PR 10-MAR-1999; 99WO-US05190.
PR PR 20-APR-1999; 99WO-US08615.
PR PR 14-MAY-1999; 99WO-US10733.
PR PR 02-JUN-1999; 99WO-US12252.
PR PR 01-SEP-1999; 99WO-US20111.
PR PR 08-SEP-1999; 99WO-US20594.
PR PR 13-SEP-1999; 99WO-US20944.
PR PR 15-SEP-1999; 99WO-US21090.
PR PR 15-SEP-1999; 99WO-US21547.
PR PR 05-OCT-1999; 99WO-US21089.
PR PR 29-NOV-1999; 99WO-US28214.
PR PR 30-NOV-1999; 99WO-US28313.
PR PR 30-NOV-1999; 99WO-US28409.
PR PR 01-DEC-1999; 99WO-US28301.
PR PR 01-DEC-1999; 99WO-US28634.
PR PR 02-DEC-1999; 99WO-US28551.
PR PR 02-DEC-1999; 99WO-US28564.
PR PR 16-DEC-1999; 99WO-US28565.
PR PR 20-DEC-1999; 99WO-US30911.
PR PR 20-DEC-1999; 99WO-US30999.
PR PR 22-DEC-1999; 99WO-US30720.
PR PR 30-DEC-1999; 99WO-US31243.
PR PR 30-DEC-1999; 99WO-US31274.
PR PR 05-JAN-2000; 2000WO-US00219.
PR PR 06-JAN-2000; 2000WO-US00277.
PR PR 06-JAN-2000; 2000WO-US00376.
PR PR 11-FEB-2000; 2000WO-US03565.
PR PR 18-FEB-2000; 2000WO-US04341.
PR PR 18-FEB-2000; 2000WO-US04342.
PR PR 22-FEB-2000; 2000WO-US04414.
PR PR 24-FEB-2000; 2000WO-US04914.
PR PR 24-FEB-2000; 2000WO-US05004.
PR PR 01-MAR-2000; 2000WO-US05601.

PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23322.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 26-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 28-DEC-2001; 2001WO-US21735.
 PR 28-FEB-2001; 2001WO-US21735.
 PR 09-MAR-2001; 2001US-0786436.
 PR 14-MAR-2001; 2001US-0802706.
 PR 22-MAR-2001; 2001US-0808689.
 PR 05-APR-2001; 2001US-0816744.
 PR 10-MAY-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0882636.
 PR 21-JUN-2001; 2001US-0886342.
 PR 18-JUL-2001; 2001US-0908879.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tamas D, Matanabe CK, Wood WI, Zhang Z;

DR WPI: 2003-331925/31.
 XX P-PSDB; AB067033.

PI New secreted and transmembrane nucleic acids and polypeptides,
 PI designated as PRO, useful for treating inflammation, organ failure,
 PI atherosclerosis, cardiac injury, infertility, birth defects, premature
 PI aging, AIDS, or cancer

XX Claim 2; Fig 375; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO

CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumor necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release of
 CC proteoglycans from cartilage, proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, RNA
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence encodes a PRO protein of the invention.

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-017-084A-523 (1-344) x ACA04211 (1-1679)

Qy	1	MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
Db	134	ATGAAACCACTCCAGCAAAATGCAAAATCTATCTCTGGCAATCTTCACGGGCTG	193
Qy	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
Db	194	GCTGCTGTGTCTCTCCAGGAGTGGCGTGGCGAGGAGTGCACCTTCCCAAA	253
Qy	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
Db	254	GCTATGGCAACCTGACGGTCCGCGAGGGGAGAGCCACCTCAGGTGCATATTGAC	313
Qy	61	AsnArgValThrArgValAlaThrIleuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80
Db	314	ACCAGGTACCCGGGTGGCTGCTTCCAGGAGTGGCGTGGCGAGGAGTGCACCTTCCCAAA	373
Qy	81	LysTrpCysIleuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle	100
Db	374	AAGTGGTCCCTGGATCTCGCTGTCTCTTCTGAGCAACCAACCAACGATCAGCATC	433
Qy	101	GluIleGlnAsnValAspValTrpAspGlnGlyProTyThrCysSerValGlnThrAsp	120
Db	434	GAGATCCAGAACCTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC	493
Qy	121	AsnHisProLysThrSerArgValHisIleuIleValGlnValSerProLysIleValGlu	140
Db	494	AACCACCAAGACCTCTAGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG	553
Qy	141	IleSerSerAspIleSerIleAsnGlnGlyValAsnAsnIleSerLeuThrCysIleAlaThr	160
Db	554	ATTTCTTCAGATATCTCCATTAATCAAGGGAACAATATTAGCTCCTCCTCATAGCAACT	613
Qy	161	GlyArgProGlnProThrValThrArgHisIleSerProLysAlaValGlyPheVal	180
Db	614	GGTAGACAGACCTACGGTACTTGGAGACACATCTCTCCCAAGAGGTTGGCTTTGTG	673
Qy	181	SerGlnAspCluTyIleuGlnGlyIleThrArgGlnGlnSerGlyAspTyGlu	200

Db 674 AGTGAAGACGAATCTGGAATTCAGGGCATCAGCCGGGAGCAGTCCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAspAspValAlaAlaProValValAlaArgValLysValThrValAsn 220
 Db 734 TGCAGTGCCTCCATGACGTCGGCCCGTGGTACGAGAGTAAAGGTCAACGCGAAC 793
 QY 221 TysProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TAICCCACATTCATTCAGAACGAGGACAGGTGACAGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAACAAGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTCAGAGAAAGAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaLysSerLys 300
 Db 974 ATCTTCTCAATGCTCTGACATGACTATGGGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCGCACCAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340
 Db 1094 AACGGCACCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1153
 QY 341 LeuLeuLysPhe 344
 Db 1154 CTCTCAATTT 1165
 RESULT 12
 ID ACA04516 standard; cDNA; 1679 BP.
 AC ACA04516;
 DT 28-MAY-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO337 DNA.
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
 KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
 KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tumour; obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis; gene; ss.
 OS Homo sapiens.
 PN US2003032062-A1.
 PD 13-FEB-2003.
 PF 01-FEB-2002; 2002US-0066273.
 PR 14-JUL-1998; 98WO-US14552.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 20-NOV-1998; 98WO-US24855.
 PR 25-NOV-1998; 98WO-US25190.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-MAR-1999; 98WO-US05028.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21347.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28365.
 PR 20-DEC-1999; 99WO-US30999.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 09-MAR-2000; 2000WO-US06471.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 15-MAY-2000; 2000WO-US13358.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-JUN-2001; 2001WO-US17443.
 PR 20-JUN-2001; 2001WO-US17800.
 PR 29-JUN-2001; 2001WO-US19692.
 PR 09-JUL-2001; 2001WO-US21066.
 PR 26-AUG-1997; 97US-056914P.
 PR 17-SEP-1997; 97US-059115P.
 PR 18-SEP-1997; 97US-059263P.
 PR 19-SEP-1997; 97US-059588P.
 PR 17-OCT-1997; 97US-062285P.
 PR 24-OCT-1997; 97US-062816P.
 PR 24-OCT-1997; 97US-063082P.
 PR 29-OCT-1997; 97US-063329P.
 PR 21-NOV-1997; 97US-063733P.
 PR 16-DEC-1997; 97US-066840P.
 PR 09-FEB-1998; 98US-074086P.
 PR 25-MAR-1998; 98US-074092P.
 PR 08-APR-1998; 98US-079294P.
 PR 10-AUG-1998; 98US-081049P.
 PR 18-AUG-1998; 98US-095998P.
 PR 09-SEP-1998; 98US-097000P.
 PR 10-SEP-1998; 98US-099601P.
 PR 10-SEP-1998; 98US-099803P.
 PR 10-SEP-1998; 98US-099811P.
 PR 17-SEP-1998; 98US-100858P.
 PR 24-SEP-1998; 98US-101922P.
 PR 20-OCT-1998; 98US-106032P.
 PR 23-NOV-1998; 98US-109304P.
 PR 15-JUN-1999; 99US-123778P.
 PR 20-JUL-1999; 99US-136959P.
 PR 26-JUL-1999; 99US-145070P.
 PR 17-AUG-1999; 99US-145698P.
 PR 07-DEC-1999; 99US-149396P.
 PR 15-NOV-2001; 2001US-0002796.
 PA (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 XX Wood WI, Zhang Z;
 XX

Thu Sep 11 16:20:52 2003

DR WPI: 2003-341963/32.
 DR P-PSDB; AB067162.
 XX New secreted and transmembrane polypeptide for modulating biological
 PT activity of a cell expressing the polypeptide, identifying agonists or
 PT antagonists of the polypeptide, and as molecular weight markers
 XX
 PS Claim 2; Fig 51; 25app; English.
 XX
 CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (II) is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or
 CC anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
 CC diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
 CC disorders, for inhibiting tumour growth, enhances vascular permeability
 CC and immune response, for inducing regeneration of auditory hair cells and
 CC for treating hearing loss in mammals, and for treating bone and/or
 CC cartilage disorders such as sports injuries and arthritis. This sequence
 CC encodes a novel human secreted and transmembrane polypeptide.
 XX
 SQ Sequence: 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:
 Pred. No.: 8.55e-167 Length: 1679
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-10-017-084A-523 (1-344) x ACA04516 (1-1679)

QY 1 MethystrhrileclnProLysMethHisAsnSerIleSerThrAlaIlePheThrGlyLeu 20
 DB 134 ATGAACACCATCCAGCCAAATGCAATTCATCTCTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTGTGTCTCTCCAGAGTGGCGGCGGAGATGCCAGCGGAGATGCCCTCCCAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyCluSerAlaThrIleuArgCysThrIleAsp 60
 DB 254 GCTATGGACACGTGACGTGCGCGGGGGGAGCGCCACCTCAGTGCACATTTAGC 313
 QY 61 AsnArgValThrArgValAlaIlePheAsnArgSerThrIleuArgAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCGGGTGGCTGGCTAACCCGACGACCATCTCTATGCTGGCAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrClnThrClnThrSerIle 100
 DB 374 AAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGACGGTGGATGGTATGACGAGGGGCGCTTACACCTGCTCGGTGCACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCCACCAAGACCTCTAGGTGCGACCTCATGTGGCAGATCTCCCAAAATCTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerIleuThrCysIleAlaThr 160

DB 554 ATTTCTCAGATATCTCCATTTATGAGGAGCAATATAGCTCCTCCTCATAGCACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGACGCTACCGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTGTG 673
 QY 181 SerGluAspClnuTyrIleuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACCAATATCTTGAATTCAGGCAATCACCCTGGGAGCAGTCCAGGGACTACGAG 733
 QY 201 CysSerIleAsnAspValAlaAlaAlaProValValAlaIleValIleValIleValAsn 220
 DB 734 TGCAGTCCCTCCCAATGACGTGCGCGCGCTGGTACGGAGACTAAAGGTCCCGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTTCAGAACCCCAAGGTACAGGTGTCCCGTGGGACAAAGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrIleAspAspLys 260
 DB 854 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTCAGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAATC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCAATGTCTCTGAACATGACTATGGGAACATACACTTGGCTGGCTCCACACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCGACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGCTCAGCGAGGTAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCAGCTCGAGGAGGCGAGGCTGCTGCTGGCTGTGCTGTGCTGTGCTGTGCTGTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165

RESULT 13
 ID ACA04996 standard; cDNA; 1679 BP.
 AC ACA04996;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
 KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
 KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tumour; obesity; diabetes; insulinaemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell; regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003032063-A1.
 XX
 PD 13-FEB-2003.
 XX
 XX 01-FEB-2002; 2002US-0066494.
 XX
 XX 14-SEP-1998; 98WO-US19093.
 PR 16-SEP-1998; 98WO-US19330.
 PR


```

Db 434 GAGATCCAGACGTTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGTGCAGACAGAC 493
Oy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 ACCACCCAAAGACCTTAGGTCACCTCATTTGGCAAGTATCTCCAAATGTAGAG 553
Oy 141 IleSerSerAspIleSerIleAsnGluIlysnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTTCAGATATCTCCATTATGAGGGAACATATATTAGCCTCACCTGCATAGCAACT 613
Oy 161 GlyArgProGluProThrValThrIleThrPargHisIleSerProLysAlaValGlyPheVal 180
Db 614 GTGACACGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
Oy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTAGCAG 733
Oy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db 734 TGCAGTGCCTCCATGACGTGGCCGCCGCTGGTACGAGAGTAAAGGTCAACGTGAAC 793
Oy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyClnLysGlyThr 240
Db 794 TATCCACCATATTCAGAAAGCAAGGGTACAGGTCTCCCGTGGACAAAGGGGACAA 853
Oy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrIleAspLys 260
Db 854 CTGCACTGTGAGCCTCAGCAGTCCCTCAGCAGAAATCCAGGTGTCACAGGTGACAA 913
Oy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerIleLeu 280
Db 914 ACACGTATGAGAAAGAAAGAGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
Oy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCCTCAATGTCCTGAACATGACTATGGAACTACATGCTTGGTGGCTGGCTGGCTGG 1033
Oy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCCCGCTCAGGAGGTGAGC 1093
Oy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGCAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1153
Oy 341 LeuLeuLysPhe 344
Db 1154 CTTCCTCAAAATTT 1165

RESULT 14
ABX89328
ID ABX89328 standard; cDNA; 1679 BP.
XX AC ABX89328;
XX DT 13-MAY-2003 (first entry)
XX DE DNA encoding novel secreted and transmembrane protein PRO337.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
XX KW cardiac insufficiency disorder; cancer; tumor; immune response;
XX KW adrenal cortical capillary endothelial growth; c-fos induction;
XX KW vascular endothelial growth factor inhibition; VEGF inhibition;
XX KW endothelial cell growth inhibitor; T-lymphocytes cell survival;
XX KW retinal neurons cell survival; rod photoreceptor cell survival;
XX KW retinal disorder; retinitis pigmentosa; kidney disorder;
XX KW mammalian kidney mesangial cell proliferation; berger disease;
XX KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
OS Homo sapiens.
```

08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-074723.
 PR 28-FEB-2001; 2000US-074623.
 PR 09-MAR-2001; 2001US-0802706.
 PR 12-MAR-2001; 2001US-0806989.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0834208.
 PR 18-MAY-2001; 2001US-0834280.
 PR 25-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0882636.
 PR 21-JUN-2001; 2001US-0886342.
 PR 18-JUL-2001; 2001US-0887879.
 PR 06-AUG-2001; 2001US-0908827.
 PR 15-AUG-2001; 2001US-0924419.
 PR 16-AUG-2001; 2001US-0927796.
 PR 19-DEC-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 PA (GETH) GENENTECH INC.
 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gerifsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR: WPI: 2003-148238/14.
 P-PSDB: AB059838.
 XX Novel isolated PRO polypeptides e.g.: PRO826, PRO1068, PRO1184, PRO1346
 PI and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 FT treatments
 XX Claim 2; Fig 375; 659pp; English.
 XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VSGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with

CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC sequence encodes a novel human PRO protein.
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
 Alignment Scores:
 Pred. No.: 8 55e-167 Length: 1679
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0
 US-10-017-084a-523 (1-344) x ABX89328 (1-1679)
 Qy 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrrAlaIlePheThrGlyLeu 20
 Db 134 ATGAAACCAATCCAGCAAAATGCAAAATCTATCTCTGGGCAATCTTCCACGGGCTG 193
 Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTGTGTCTCTTCCAAAGAGTGCCTGCGAGGAGATGCCACCTTCCCAAAA 253
 Qy 41 AlaMetAspAsnValThrValArgGlnGlySerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGGACAACGTCGCTCCGAGGAGGAGAGCCACCTCAGGTGCACATATTGAC 313
 Qy 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuThrAlaGlyAsnAsp 80
 Db 314 AACCGGTTCACCGGCTGGCTAAACCGCAGCACCATCTCTATGTTGGTAATGAC 373
 Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlyThrSerIle 100
 Db 374 AAGTGGTGGCTGGATCTCGCTGCTCTTCTGAGCAACACCAACAGCAGTACAGCATC 433
 Qy 101 GluIleGlnAsnValAspValThrValArgGlnGlySerValThrCysSerValGlnThrAsp 120
 Db 434 GAGATCCAGAACGTGGATGTATCAGCGGGCCCTTACACCTCTGCTGCGACAGAC 493
 Qy 121 AsnHisProLysThrSerArgValHisLeuLeuValGlnValSerProLysIleValGlu 140
 Db 494 AACCAACCAAGACCTCTAGGTCACCTCATTTGCAAGTATCTCCCAAAATTTGATAG 553
 Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTTCTTCAGATATCTCCATTAAAGAGGAACAAATATTAGCCTCACCTGCATAGCACT 613
 Qy 161 GlyArgProGluProThrValThrIleArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGCCAGAGCTACGCTTACTTTGGAGACACATCTCTCCCAAGCGTTGGTGTGTG 673
 Qy 181 SerGluAspGluTrpLeuGluIleGlnGlyIleThrArgGlnGlnSerGlyAspTrpGlu 200
 Db 674 AGTGAAGACGAATACTTTGGAATTCAGGCACTACCCGGGAGCAGTACGAGTACGAG 733
 Qy 201 CysSerAlaSerAspAspValAlaAlaProValValArgValValValValValAsn 220
 Db 734 TGCAGTGCCTCCATGACGCTGGCGCGCGCTGGTACGGAGAGTAAAGGTCCACGTGAAC 793
 Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATATCTTTCAGAGCCAAAGGTGTACAGGTCTCCCGTGGGCAAAAGGGACA 853
 Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCCAGCAATTCAGTGTGTACAGGATGACAAA 913
 Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280

cartilage disorders and immune deficiencies

Claim 2; Fig 221; 459pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The bioactive molecule may be a toxin, radiolabel or antibody, and causes apoptosis or death of the cell. The PRO polypeptides are useful for treating immune disorders, diabetes or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system disorders, kidney disorders, bone and cartilage disorders or arthritis, tumours, and wound healing. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. The present sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/ps/pdIDEntry.html.

XX SC Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8,55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-017-084A-523 (1-344) x ABX92696 (1-1679)

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QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GTGCTCTGTGTCTTCCCAAGAGGTGCCCGCGGAGAGATGCCACCTTCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluserAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCATTTGAC	313
QY	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCCTCTCTATGCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AAGTGTGCTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC	433
QY	101	GlutLeuGlnAsnValAspValTyrAspGlyProTyrThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGACGTGGATGTGTATGACAGAGGGCCCTACACCTGCTCGGTGAGACAGAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACACCCCAAGACCTCTAGGGTCCACCTCAITGTGCAAGTATCTCCCAAAATTTAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTCTCTCAGATATCTCCATTAAATGAAGGACACATATTAGCCCTCACCTGATGCAACT	613
QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
DB	614	GGTAGACACGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	673

Search completed: September 11, 2003, 03:13:59

Job time : 379 secs

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QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220
DB	734	TGACGTGCTCCCAATGACCTGGCGCGCGCTGTAGCGAGAGTAAAGTCCACGTGAAC	793
QY	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlyLysGlyThr	240
DB	794	TATCCACCATACATTTTCAGAACCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA	853
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys	260
DB	854	CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGATTCAGTGGGTACAGGATGACAAA	913
QY	261	ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
DB	914	AGACTGATTTGAAGAAAGAGGGGTGAAGTGAAGAACAGACCTTCTCTCAAAACTC	973
QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
DB	974	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGGGTGGCTCCCAACAG	1033
QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
DB	1034	CTGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGCTCAGCGAGGTGAGC	1093
QY	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu	340
DB	1094	AACGCGACGTGAGGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1153
QY	341	LeuLeuLysPhe	344
DB	1154	CTTCTCAATTT	1165

GenCore version 5.1.6
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Run on: September 11, 2003, 03:14:04 ; Search time 93 Seconds
(without alignments)
1632.643 Million cell updates/sec

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Perfect score: 1806
Sequence: 1 MKTIOPKHNSISWAIFTGL.....RRAGCVMLLPVLVHLLKLF 344

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 569578 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	926.5	51.3	1014	2	US-08-414-657D-5
2	926.5	51.3	1014	4	US-09-135-080-7
3	926.5	51.3	1238	2	US-08-414-657D-3
4	926.5	51.3	1238	4	US-09-135-080-3
5	923.5	51.1	977	2	US-08-414-657D-1
6	923.5	51.1	977	4	US-09-135-080-1
7	908	50.3	924	2	US-08-414-657D-7
8	907	50.2	945	2	US-08-414-657D-8
9	902	49.9	912	2	US-08-414-657D-6
10	896.5	49.1	861	2	US-08-414-657D-9
11	895.5	49.0	861	2	US-08-414-657D-10
12	796.5	44.1	756	2	US-08-414-657D-17

13	795.5	44.0	756	2	US-08-414-657D-18
14	263.5	14.6	6814	4	US-09-484-970B-66
15	256	14.2	1266	2	US-08-639-984A-2
16	256	14.2	1266	3	US-08-639-984A-4
17	256	14.2	1335	3	US-08-639-984A-4
18	256	14.2	1335	3	US-08-639-984A-4
19	246.5	13.6	3360	1	US-08-408-093-5
20	246.5	13.6	3360	1	US-08-408-420A-5
21	246.5	13.6	3360	1	US-08-714-901-5
22	246.5	13.6	3360	3	US-08-040-741-5
23	237	13.1	219	2	US-08-414-657D-11
24	237	13.1	219	2	US-08-414-657D-12
25	230.5	12.8	2869	1	US-08-374-834-2
26	230.5	12.8	2869	1	US-08-644-271-2
27	230.5	12.8	2869	4	US-09-077-955-2
28	230	12.7	2610	1	US-08-374-834-17
29	230	12.7	2610	1	US-08-644-271-28
30	230	12.7	2610	1	US-09-077-955-32
31	225.5	12.5	1581	5	PC1-US95-08493-14
32	225.5	12.5	2580	5	PC1-US95-08493-18
33	225.5	12.5	2604	5	PC1-US95-08493-20
34	220.5	12.2	1598	4	US-09-778-510-19
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36	219	12.1	4843	3	US-08-986-485-1
37	213.5	11.8	1718	4	US-09-778-510-5
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41	209	11.6	3402	4	US-09-998-243-118
42	205.5	11.4	1542	4	US-09-205-258-123
43	205.5	11.4	1820	4	US-09-778-510-1
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45	203.5	11.3	5824	4	US-09-620-312D-72

ALIGNMENTS

RESULT 1
US-08-414-657D-5
; Sequence 5: Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
1 APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:

Score: 926.50 Matches: 179
 Percent Similarity: 73.54% Conservative: 60
 Best Local Similarity: 55.08% Mismatches: 81
 Query Match: 51.30% Indels: 5
 DB: 4 Gaps: 4

US-10-017-084a-523 (1-344) x US-09-135-080-7 (1-1014)

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 DB CTGAGACTGCTCTCCCTTCTCCACAGACTGCGCGTTCGACGCTGGAT-----TTT 102

QY 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
 DB AACCAGGAGCAGCAACATCACCCTGAGCGAGGGGACACGGCCATCTCAGGTGTGTG 162

QY 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrrAlaGly 78
 DB GTAGAAGACAAGAACTCGAAAGTGGCTGTGTGAACCGCTCTGCATCATCTCGCTGA 222

QY 79 AsnAspLysTTPCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGly 98
 DB CAGCAAGTGGTCTCTGGACCTCGGTGGTGGAGAACGCCATGCTCTGGAATAC 282

QY 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
 DB AGCTCCGAAATCCAGAGGTGGATGCTATGATGAGATCCACATGCTCAGTTCNG 342

QY 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
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QY 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
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QY 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
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QY 259 AspLysArgLeuIleGluGlyLysLysValLysValGluAsnArgProPheLeuSer 278
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RESULT 3
 US-08-414-657D-3
 ; Sequence 3, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,657D
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1238 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 56...1069
 ; OTHER INFORMATION:
 ; US-08-414-657D-3

Alignment Scores:
 Pred. No.: 6.2e-99 Length: 1238
 Score: 926.50 Matches: 179
 Percent Similarity: 73.54% Conservative: 60
 Best Local Similarity: 55.08% Mismatches: 81
 Query Match: 51.30% Indels: 5
 DB: 4 Gaps: 4

US-10-017-084a-523 (1-344) x US-08-414-657D-3 (1-1238)

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QY 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrrAlaGly 78

458	TCCAACATCTCCCGGATGTCAC	TGTGATGAGGGCAGCAATGTA	ACCCTGGTCTGCATG	517
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638	TATGAGTGCACGCGTCCAA	CGAGGTCTCTCCGCGGAT	GTCAAAACAAAGTCAAGGTCACT	697
Qy	ValAsnTyrProTyrIleSer	GluAlaLysGlyThrGly	ValProValGlyGlnLys	238
Db				
698	GTGAACATTCCACCCACCAT	CACAGAGCTTAGAGCAAT	GAAAGCCACACAGCAGCAGCA	757
Qy	GlyThrLeuGlnCysGluAla	SerAlaValProSerAla	GluPheGlnTyrTyrLysAsp	258
Db				
758	GCTTCCCTCAAAATGTGA	AGCCTCAGCGGTGCTCTG	CACCTGACTTTGAGTGGTACGGGAT	817
Qy	AspLysArgLeuIleGluGly	LysLysGlyValLysVal	GluAsnArgProPheLeuSer	278
Db				
818	GACACACAGG---ATAAAC	AGTGCACAAAGCCCTTGAG	ATTAAAGACACTGAGGCGCCAGTCC	874
Qy	LysLeuIlePhePheAsnVal	SerGluHisAspTyrGly	AsnTyrThrCysValAlaSer	298
Db				
875	TCCCTGCAGCGTGACCA	AGCTCCTCAGGGAAACACT	CAGGCAACTATACCTGTGTGGTGCC	934
Qy	AsnLysLeuGlyHisThr	AsnAlaSerIleMetLeu	PheGlyProGlyAlaValSerGlu	318
Db				
935	AACAAGCTCGGGGTCC	CAAAATGCCAGCGTAGT	CCCTTTTCACACCCGGGTGGTGAGAGGA	994
Qy	ValSerAsnGlyThrSer	ArgArgAlaGlyCysVal	TyrPheLeuProLeuLeuValLeu	338
Db				
995	ATC---AACGGATCC	ATCAGTCTGGCCGTACC	ACTGTGGCTGGCAGCGGTCCCTGTTC	1051
Qy	HisLeuLeuLys	343		
Db				
1052	TGCTTCTTCAGCAAA	1066		

·RESULT: 5

US-08-414-657D-1
; Sequence 1, Application US/08414657D

; PATENT NO. 3661263
; GENERAL INFORMATION:

GENERAL INFORMATION: .
APPLICANT: Levitt, pat .

APPLICANT: Levitt, Pat
APPLICANT: Pimenta Aurora

APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak

; APPLICANT: Zhukareva, Victoria

; TITLE OF INVENTION: Limbic System-A

TITLE OF INVENTION: PROTECTOR

TITLE OF INVENTION: FI
 :
 :
 NUMBER OF SEQUENCES: 6

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

;
; ADDRESS: Doobert Drive, Phoenix

; ADDRESS:

STREET: 9

; CITY: Lawren

STATE: NJ

STATE: NO
COUNTRY: USA

COUNTRY: USA
ZTP: 08543

ZIP: 08543
COMPUTER READABLE FORM.

; COMPUTER READABLE FORM:

```

;
; MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatib

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows, Vers

; SOFTWARE: FASUSEQ IO
; CURRENT APPLICATION DAT

APPLICANT NUMBER:

APPLICATION NUMBER: 33 432 100

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 2...976
OTHER INFORMATION:
US-08-414-657D-1
Alignment Scores:
Pred. No.: 9,62E-99
Score: 923.50
Percent Similarity: 74.06%
Best Local Similarity: 55.31%
Query Match: 51.14%
DB: 2
Length: 977
Matches: 177
Conservative: 60
Mismatches: 78
Indels: 5
Gaps: 4

[illegible]

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 945 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...945
 OTHER INFORMATION:

US-C8-414-657D-8

Alignment Scores:
 Pred. No.: 7.87e-97 Length: 945
 Score: 907.00 Matches: 170
 Percent Similarity: 75.50% Conservative: 58
 Best Local Similarity: 56.29% Mismatches: 70
 Query Match: 50.22% Indels: 4
 DB: 2 Gaps: 3

US-10-017-084a-523 (1-344) x US-08-414-657D-8 (1-945)

Cy 20 LeuAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAlaThrPhe 38
 Db 49 CTGAGACTGCTCTGCTCTTCCACAGGACTGCGCTTCGACGGTGGAT-----TTT 102
 Cy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
 Db 103 AACCGAGCGACGACAAACATCACCCTGAGCGAGGGGACACGCCCATCTCAGGTGTG 162
 Cy 59 IleAspAsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyAlaGly 78
 Db 163 GTAGAAGACAGAACTCGAAAGTGGCTGTGTAACCGCTCTGGCATCATCTTCGTGA 222
 Cy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGln 98
 Db 223 CACGACAGTGGTCTCTGGACCTCGGCTGAGCTGGAGAACGCCATCTCGAATAC 282
 Cy 99 SerIleGluIleGlnAsnValAspValArgGlnGlyProTyThrCysSerValGln 118
 Db 283 ACCCTCCCAATCCAAAGGTGGTGTCTATGATGAAGATCCCTACACATGCTCAGTTCAG 342
 Cy 119 ThrAspAsnHisProLysThrSerArgValHisLeuValGlnValSerProLysIle 138
 Db 343 ACACAGCATAGGCCCAAGACCTCTCAAGTTTACTTGTATTGATGACAAAGTCCACAAATC 402
 Cy 139 ValGluIleSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIle 158
 Db 403 TCCAAATCTCTCGGATGTCTACTGTGAATGAGGCGACCAATTAACCTGCTGTCATG 462
 Cy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
 Db 463 GCCAATGGCGCCCTGAACCTGTATACCTGGAGACACCTTACACCATCTGGAGAGAA 522
 Cy 179 PheValSerGluAspGluTrpLeuGluIleGlnGlyThrArgGluGlnSerGlyAsp 198

Db 523 TTGAAGGAGAAGAATAATCTGGAGATCTTAGGCATCACCAGGGAACATCAGGCAA 582
 Cy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValArgValValValThr 218
 Db 583 TATGAGTGCAAGGCTGCCAACAGAGTCTCTCCCGCGATGTCACAAAGTCAAGGTCACT 642
 Cy 219 ValAsnTrpProTyThrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
 Db 643 GTGAAGTATCCACCCACCATCAGAGTCTAAGAGCAATGAAGCAACCCACAGGACGAA 702
 Cy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLysAsp 258
 Db 703 GCTTCCCTCAATGTGAAGCTCAGCGGTGCTGCACCTGACTTTGAGTGTGTCGGGAT 762
 Cy 259 AspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
 Db 763 GACACACAGG--ATAAACAGTCAAACGGCTTGAGATTAGAGCACTGAGGCGCAGTCC 819
 Cy 279 LysLeuIlePhePheAsnValSerGluHisAspTyGlyAsnTyThrCysValAlaSer 298
 Db 820 TCCCTGAGCGTGACCAACGCTCAGTGAAGACACTACGCACTATACCTGTGTGCTGCC 879
 Cy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
 Db 880 AACAGCTCGGCTCACCACCACTCCAGCTAGTCTCTTTTTCAGACCCGCGGTGAGAGGA 939
 Cy 319 ValSer 320
 Db 940 ATCAAC 945

RESULT 9

US-08-414-657D-6
 Sequence 6, Application US/08414657D
 Patent No. 5861283
 GENERAL INFORMATION:
 APPLICANT: Levitt, Pat
 APPLICANT: Pimenta, Aurea
 APPLICANT: Fischer, Itzhak
 APPLICANT: Zhukareva, Victoria
 TITLE OF INVENTION: Limbic System-Associated Membrane
 TITLE OF INVENTION: Protein and DNA
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESS: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 912 base pairs


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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..912
; OTHER INFORMATION:
US-08-414-657D-6
Alignment Scores:
Pred. No.: 2,87e-96 Length: 912
Score: 902.00 Matches: 171
Percent Similarity: 74.68% Conservative: 59
Best Local Similarity: 55.52% Mismatches: 74
Query Match: 49.94% Indels: 4
DB: 2 Gaps: 3
US-10-017-084A-523 (1-344) x US-08-414-657D-6 (1-912)
QY 31 ValArgSerGlyAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
DB 1 GTTCGACGCTGGAT-----TTTAACCGAGGCGACACATCACCGTGAGGCGG 54
QY 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaLeu 70
DB 55 GACACACCCATCTCAGGTGGCTTAGAGACAGCAACTCAAGGTGGCTGGTGAAC 114
QY 71 ArgSerThrIleLeuValAlaGlyAsnAspLysTrpCysLeuAspProArgValLeu 90
DB 115 CGTCTGGCATCATTTTCTGGACATGACAGTGTCTCTGGACCCAGGTTGAGCTG 174
QY 91 LeuSerAsnThrGlnThrGlnTySerIleGluLeuIleGlnAsnValAspValTyrAspGlu 110
DB 175 GAGAAAGCCATCTCTGGAATACAGCTCCGATCCAGAGGTGGATGTCTATGATGAG 234
QY 111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
DB 235 GTTCTTACACTTGTCTGAGTTCAGACACAGCAGTCCGACCCAGACCTCCCAAGTTACTTG 294
QY 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
DB 295 ATCTGACAAAGTCCCAAGATATCCCGATGATGATGATGATGATGATGATGATGATG 354
QY 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
DB 355 AGCAACGTGACTGTGTCTGATGCGCAATGCGGCTGCTGAACCTGTATCACCTGAGAG 414
QY 171 HistIleSerProLysAlaValGlyPheValSerGluAspLysLeuGlnGly 190
DB 415 CACCTTACACCAACTGGAAGGGAATTTGAAGGAGGAAGAATACTCGAGATCCTTGGC 474
QY 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAspAspValAlaAlaPro 210
DB 475 ATCCAGGAGGAGCAGTCAGCAATATGAGTGCAGAGTCCCAAGCTGCTCTCGGCG 534
QY 211 ValValArgValLysValThrValAsnTyrProTyrIleSerGluAlaLysGly 230
DB 535 GATCTCAACAGCTCAAGTCTGTAATCTTCCCACTATCCAGATCCAGATCCAGAGC 594
QY 231 ThrGlyValProValGlyGlnIleGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
DB 595 ANTGAAGCCACCCAGGAGCAGCTCACTCAATGAGGAGGCTCGGCGTGGCTGCA 654
QY 251 AlaGluPheGlnTrpTyrIleAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
DB 655 CCGTACTTGGTGGTACCGGATGACACTAGG---ATAAATAGTGCATGCGCTGAG 711
QY 271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
DB 712 ATTAAGACGAGGAGGCGGCTCTCCCTGACGCTGACCAAGCTCACTGAGGAGCACTAC 771
QY 291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAspAlaSerIleMetLeu 310
DB 31 ValArgSerGlyAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50

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DB 772 GGCAACTACACCTGTGTGGCTGCCAACACAGCTGGGGTGCACCATGCCCTAGTCTCTT 831
QY 311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
DB 832 TTCAGCTGGTGGTGGTGGAGGAATA---AATGATCATCATGCTCGGCGTACCACCTG 888
QY 331 TrpLeuLeuProLeuLeuValLeu 338
DB 889 TGGCTGTGGCAGCATCTCTGCTC 912
RESULT 10
US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...861
; OTHER INFORMATION:
US-08-414-657D-9
Alignment Scores:
Pred. No.: 1,73e-94 Length: 861
Score: 886.50 Matches: 164
Percent Similarity: 76.21% Conservative: 57
Best Local Similarity: 56.55% Mismatches: 66
Query Match: 49.09% Indels: 3
DB: 2 Gaps: 2
US-10-017-084A-523 (1-344) x US-08-414-657D-9 (1-861)
QY 31 ValArgSerGlyAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
DB 31 ValArgSerGlyAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50

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Db 1 GTTCCAGCGTGGAT-----TTTAACCGAGGACGAGACACATCACCGTGAGCGAGGG 54
 Qy 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
 Db 55 GACACGCCATCTCAGTGGCTTCTAGACAGCAAGCACTCAAGTGGCTGTGGTGAAC 114
 Qy 71 ArgSerThrIleLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeu 90
 Db 115 CTTCTGGCATCATCTTCTGACATCAAGTGGTCTCTGACCCACCGGTGTGAGCTG 174
 Qy 91 LeuSerAsnThrGlnThrGlnTyrSerIleGluLeuIleGlnAsnValAspValTyrAspGlu 110
 Db 175 GAGAAAGCCATCTCTGGAATACAGCTCCGAAATCCAGAAAGTGGATGTCTATGATGAG 234
 Qy 111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
 Db 235 GGTCTCTACACTTCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTG 294
 Qy 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
 Db 295 ATCTGTACAAAGTCCCAAGATCTCCAAATATCTCTCGGATGTCACGTGTGAATGAGGCG 354
 Qy 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
 Db 355 AGCAACGTGACTCTGTCTGATGGCCAAATGGCGCTCTGAACCTGTGTATCACCTGGAGA 414
 Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
 Db 415 CACCTTACACCACTGGAGGGAATTTGACGACAGCAAGCAATATCTGGAGTCTTGGC 474
 Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspAlaAlaPro 210
 Db 475 ATCACCAGGAGCAGTCAGGCAATATGATGCAAGTCTCCCAAGTCTCTCGGCG 534
 Qy 211 ValValArgValIleValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
 Db 535 GATGTCAACCAAGTCAAGTCTGATGCAATATCTCTCCCAATATCAAGATCCCAAGAGC 594
 Qy 231 ThrGlyValProValGlyGlnIleGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
 Db 595 AATGAAGCCACACAGCAGCAGCAAGTCTCACTCAATGATGAGCCCTCGGAGTCCCTGCA 654
 Qy 251 AlaGluPheGlnTyrIleAspAsnLysArgLeuIleGluGlyLysGlyValIle 270
 Db 655 CTTGACTTGTAGTGGTACCGGATGACACACTAGG---ATAAATAGTGGCAATGGCTTGAG 711
 Qy 271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
 Db 712 ATTAAGACGAGGAGGCGGCTCTCTCCCTGACGCTGACCAACCTCACTGAGGAGCACTAC 771
 Qy 291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
 Db 772 GCACTACACTGTGTGGCTGCCAACAAGCTGGGGGTACCAATGCCAGCTAGTCTCT 831
 Qy 311 PheGlyProGlyAlaValSerGluValSer 320
 Db 832 TTCAGACCTGGTGGTGGTGGAGAGCAATTAAT 861

RESULT 11

US-08-414-657D-10
 : Sequence 10, Application US/08414657D
 : Patent No. 5861283
 : GENERAL INFORMATION:
 : APPLICANT: Levitt, Pat
 : APPLICANT: Pimenta, Aurea
 : APPLICANT: Fischer, Itzhak
 : APPLICANT: Zhukareva, Victoria
 : TITLE OF INVENTION: Limbic System-Associated Membrane
 : NUMBER OF SEQUENCES: 60
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dechert Price & Rhoads
 : STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville
 STATE: NY
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ FOR Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 861 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...861
 OTHER INFORMATION:
 US-08-414-657D-10
 Alignment Scores:
 Pred. No.: 2,26e-94 Length: 861
 Score: 885.50 Matches: 184
 Percent Similarity: 76.21% Conservative: 57
 Best Local Similarity: 56.55% Mismatches: 66
 Query Match: 49.03% Indels: 3
 DB: 2 Gaps: 2
 US-10-017-084A-523 (1-344) x US-08-414-657D-10 (1-861)
 Qy 31 ValArgSerGlyAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
 Db 1 GTTCCAGCGTGGAT-----TTTAACCGAGGACGAGACACATCACCGTGAGCGAGGG 54
 Qy 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
 Db 55 GACACGCCATCTCAGTGGCTTCTAGACAGCAAGCACTCAAGTGGCTGTGGTGAAC 114
 Qy 71 ArgSerThrIleLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeu 90
 Db 115 CTTCTGGCATCATCTTCTGACATCAAGTGGTCTCTGACCCACCGGTGTGAGCTG 174
 Qy 91 LeuSerAsnThrGlnThrGlnTyrSerIleGluLeuIleGlnAsnValAspValTyrAspGlu 110
 Db 175 GAGAAAGCCATCTCTGGAATACAGCTCCGAAATCCAGAAAGTGGATGTCTATGATGAG 234
 Qy 111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
 Db 235 GGTCTCTACACTTCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTG 294
 Qy 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
 Db 295 ATCTGTACAAAGTCCCAAGATCTCCAAATATCTCTCGGATGTCACGTGTGAATGAGGCG 354
 Qy 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
 Db 355 AGCAACGTGACTCTGTCTGATGGCCAAATGGCGCTCTGAACCTGTGTATCACCTGGAGA 414

RESULT 13
 US-08-414-657D-18
 ; Sequence 18, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Lambic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-5214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 756 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 1..756
 ; OTHER INFORMATION:
 ; US-08-414-657D-18
 ;
 Alignment Scores:
 Pred. No.: 6,678-84 Length: 756
 Score: 795.50 Matches: 144
 Percent Similarity: 76.68% Conservative: 50
 Best Local Similarity: 56.92% Mismatches: 58
 Query Match: 44.05% Indels: 1
 DB: 2 Gaps: 1
 ;
 US-10-017-084A-523 (1-344) x US-08-414-657D-18 (1-756)
 QY 50 GlycylSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeu 69
 Db 1 GGGGACAGCGCCATCTCTAGGTGTGTGTAGACACAGAACTCGAAAGTGGCTGTG 60
 QY 70 AsnArgSerThrIleLeuArgCysThrIleAspAsnArgValThrArgValAlaVal 89
 Db 61 AACCGCTCTGGCATCATCTCTGGACACAGAACTGTCTGGACCCCTCGGGTTGAG 120
 QY 90 LeuLeuSerAsnThrGlnThrGlnThrSerIleGlnAsnValAspValThrAsp 109
 Db 121 CTGGAGAAAGCCCATCTCTGGAATACAGCTCGGATCCAGAAAGTGGATGTCTATGAT 180

QY 110 GluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHis 129
 Db 181 GAAGATCTTACACATCTCAGTCACACAGCATGAGCCCAAGACCTCTCAAGTTTAC 240
 QY 130 LeuIleValGlnValSerProLysIleValGlnIleSerSerAspIleAsnGlu 149
 Db 241 TTGATTGTACAGTTTCCACCAAGATTCCTCAACATCTCTCGATGTCTCTGTATGAG 300
 QY 150 GlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrp 169
 Db 301 GGCAGCAATGTAACTCTGTCTGATGCCAATGGGCCCTTGAACCTGTATCACCCTGG 360
 QY 170 ArgHisIleSerProLysAlaValGlyPheValSerGluAspGlyLeuGluIleGln 189
 Db 361 AGACACCTTACACCACTTGGAGAGAAATTTGAAGGAGAGAAAGATATCTCGAGATCCTA 420
 QY 190 GlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAla 209
 Db 421 GGCATCACCAGGAGACAGTCAGGCAAAATATGATGCAAGGCTGCCAAGAGGTCTCTCC 480
 QY 210 ProValValArgArgValLysValThrValAsnTyrProTyrIleSerGluAlaLys 229
 Db 481 CGGATGTCAACCAAGTCAAGTCTGATGATATCCACCATCATCAGAGTCTAAG 540
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 ; Patent No. 6426186
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 ; APPLICANT: Jones, Karen A.
 ; APPLICANT: Volkmut, Wayne
 ; APPLICANT: Walker, Michael G.
 ; TITLE OF INVENTION: BONE REMODELING GENES
 ; FILE REFERENCE: PB-0014 US
 ; CURRENT APPLICATION NUMBER: US/09/484,970B
 ; CURRENT FILING DATE: 2000-01-18
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GenCore version 5.1.6
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Title: US-10-017-084A-523

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
US-09-978-295A-522
Sequence 522, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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RESULT 2
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 ; Patent No. US20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Olang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
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 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C27
;; CURRENT APPLICATION NUMBER: US/09/978,697
;; CURRENT FILING DATE: 2001-10-16
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;; PRIOR APPLICATION NUMBER: 60/079689
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;; PRIOR FILING DATE: 1998-04-15
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;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
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;; PRIOR FILING DATE: 1998-04-23
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;; PRIOR FILING DATE: 1998-04-28
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;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR APPLICATION NUMBER: 60/084366
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;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627

; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
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 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 9,94e-216 Length: 1679
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-697-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerThrAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCCAAATATGACAAATCTATCTCTTGGCCATCTTCACGGGCGTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTGCTGCTCTTCACAGAGTGCCGTCGCGAGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyCysLeuAlaThrLeuArgCysThrIleAsp 60
 DB 234 GCTATGACAACTGACGCTCCGCGAGGGGAGGAGCCACCTCAGGTGCATTTGAC 313
 QY 61 AsnArgValThrArgValAlaThrIleAsnArgSerThrIleLeuTyfAlaGlyAsnAsp 80
 DB 314 AACCGGTACACCGGTGCGCTAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyfSerIle 100
 DB 374 AAGTGGTGCTGATCCTCGGTGCTCTTCGAGCAACCAACCAACCAACCAACCAACCA 433
 QY 101 GluIleGlnAsnValAspValTyfAspGluGlyProTyfThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACCTGATGTATGACGAGGGGCTTACACCTGCTGCTGCTGCTGCTGCTG 493
 QY 121 AsnHisProLysThrSerArgValHisIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTCTAGGCTCCACCTCATTTGTCAGAGTATCTCCCAAAATTTGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluCysLeuAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTCTTCAGATATCTCCATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673
 QY 181 SerGluAspGluTyfLeuGluIleGlnGlyLeuThrArgGluGlnSerGlyAspTyfGlu 200

DB 674 AGTGAAGACGATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGAGTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValValVal 220
 DB 734 TGCAGTGCCTCAATGACGTGCGCGCCGCGTACGAGAGTAAAGGTACCGTGAAC 793
 QY 221 TyrProProTyfIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATCATTCAGAGCCAGGTTACAGGTGTCCTCCGCGGACAAAAGGGGAC 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyfLysAspAspLys 260
 DB 854 CTGCGTGTGAGAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGTGACAGATGACAAA 913
 QY 261 ArgIleGluGlyLysGlyValLysValLysValLysValLysValLysValLysVal 280
 DB 914 AGACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 973
 QY 281 IlePhePheAsnValSerGluHisAspTyfGlyAsnTyfThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCAATGCTCTCTGAACATGACTATGGAACATACACTTGGTGGCTCCACAA 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluVal 320
 DB 1034 CTGGCCACACCAATGCCAGCATCATCTATTGGTCCAGGCGCGTCCAGGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
 QY 341 LeuLeuTyfPhe 344
 DB 1154 CTCTCAATTT 1165

RESULT 3

US-09-978-192A-522
 Sequence 522 Application US/09978192A
 Patent No. US2002017553N1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Sheiton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630P1C9
 CURRENT APPLICATION NUMBER: US/09/978,192A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
 Pred. No.: 9, 94e-216 Length: 1679
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-192A-522 (1-1679)

QY 1 MetlyThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAACCAATCCAGCAAAATGCACAATCTCTCTGTGGCAATCTTCACGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTGTGTCTCTCCAAAGGAGTGCCTGCGCAGGAGAGTCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGACAACTGACGCTCCGCGCAGGGAGAGCGCCACCTCAGGTGACTATTGAC 313
 QY 51 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuValArgIleAsnAsp 80
 DB 314 ACCGGGTACCCGGGTGCTGCTGCTTAACCGCAGCACCCTCTATGTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrIleSerIle 100
 DB 374 AGTGTGTGCTGATCTCGCTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValThrArgGlyProGlyProGlyProGlyProGlyProGly 120
 DB 434 GAGATCCAAAGCTGGATGCTATGACGAGGGGCTTACACCTGCTGCTGCTGCTGCTGCT 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCCCAAAAGCTCTAGGCTCCACTTATGTGCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGlnGlyAspAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCAGCTCAGTACGAC 613
 QY 161 GlyArgProGlnProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGCTTACCTGTTGAGACATCTCTCCCAAGGGTGGCTTTG 673
 QY 181 SerGluAspGlyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
 DB 674 AGTGAAGACGAATCTTGAATTCAGGGCATCACCAGGAGCAGTACGGGGGACTACGAG 733
 QY 201 CysSerAlaSerAspValAlaAlaProValValArgValValValThrValAsn 220
 DB 734 TGCAGTGCCTCAATGACGTGCGCGCTGGTACGAGAGTAAGAGTACCGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240

DB 794 TATCCACCATACATTTCCAGAACCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260
 DB 854 CTGCAAGTGTGAAGCTCCAGCAGTCCCTCAGCAGAAATTCAGTGTGATCAAGGATGACAA 913
 QY 261 ArgLeuIleGlnGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAACAAAGGGTCAAAAGTGAAGAACACAGACCTTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCAATGTCTCTGAACATGACTATGGGAACACTACTTGGTGGCTCCACAAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGCCACACCAATGCCAGCATCATCTATTTGGTCCAGGCGGCTCAGGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCACCTCGAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTTCTCAAAATTT 1165

RESULT 4

US-09-999-832A-522
 ; Sequence 522, Application US/0999832A
 ; Publication No. US20020192706A1
 GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Garber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC63
 CURRENT APPLICATION NUMBER: US/09/999,832A
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364

[illegible]

; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 9,946-216 Length: 1679
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-999-832A-522 (1-1679)

Qy	1	MetLysThrIleGlnProLysMetHisAsnSerIleSerTTPAlaIlePheThrGlyLeu	20
Db	134	ATGAAACCATCCAGCCAAAATGACATTTCTTGTGGCAATCTTCACGGGGCTG	193
Qy	21	AlaAlaLeuLysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
Db	194	GCTGCTCTGTCTCTTCCAAAGAGTGGCCGCGGAGGAGATGCCACCTTCCCAAA	253
Qy	41	AlaMetAspValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
Db	254	GCTATCGAACAAGTACGGTCCGCGAGGGGAGAGCCACCTTCAGGTGCATATTGAC	313
Qy	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80
Db	314	AACCGGGTCCCGGGTGGCTGGCTTCTGAGCAACACCCAGCAGTACGATC	373
Qy	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle	100
Db	374	AGTGGTGGCTGGATCTCGCGTGGCTCTGAGCAACACCCAGCAGTACGATC	433
Qy	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
Db	434	GACATCCAGAGTGGATGTGTATGAGAGGGCCCTACACCTCGGTGAGACACAC	493
Qy	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
Db	494	AACCAACCAAGACCTTAGGGTCCACCTATGTGCAAGTATCTCCAAATTTGAGAG	553
Qy	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
Db	554	ATTCTTCAGATATCTCCATTAATGAAGGGAACATATTAGCCCTACCTGCATAGCACT	613
Qy	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
Db	614	GTPAGACAGAGCCTTACGGTACTTGGAGACACATCTCTCCAAAGCGTGGCTTTGTG	673
Qy	181	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlnGlnSerGlyAspTyrGlu	200
Db	674	AGTGAAGCAATACTTGGAAATTCAGGGCATCACCGGGAGCAGTACGGGACTACGAG	733
Qy	201	CysSerAlaSerAsnAspValAlaAlaProValValArgValGlyValThrValAsn	220
Db	734	TGCAGTGCCTCCATGACGTGGCGCCCGCTGTGTCGAGAGATGAAGTCCACCTGAC	793
Qy	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
Db	794	TATCCACCATCATTTCAAGGCAAGGATGAGTGTCCCGGAGGCAAAAGGGGACA	853
Qy	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys	260
Db	854	CTGCAAGTGTGAAGCCTCAGCAGTCCCTCCCTCAGCAGAAATTCAGGTGATCAAGATGACAAA	913

RESULT 5

US-09-978-189-522
 ; Sequence 522, Application US/09978189
 ; Publication No. US20030004102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavon, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC7
 ; CURRENT APPLICATION NUMBER: US/09/978,189
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077641
 ; PRIOR FILING DATE: 1998-03-11

Qy	261	ArgLeuIleGluGlyLysLysGlyValGlyValGluAsnArgProPheLeuSerLysLeu	280
Db	914	AGACTGATTGAAGGAAGAAGGGTGAAGTGGAAACAGACCTTTCTCTCAAACTC	973
Qy	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
Db	974	ATCTCTCAATGTCTCTGACATGACTATGGGAACACTACCTGCGTGGCTCCAAACAG	1033
Qy	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
Db	1034	CTGGGCACACCAATGCCAGCATCATCTATTGGTCCAGGCGCGTCAGGAGGTGAC	1093
Qy	321	AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu	340
Db	1094	AACGGCACGTCGAGGAGGCGAGCTGCGTCTGCTGCTCTCTTCTGCTTTGCACCTG	1153
Qy	341	LeuLeuLysPhe	344
Db	1154	CTTCTCAATTT	1165

[illegible]

; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 9,94e-216 Length: 1679
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-189-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCAACCCAGCCAAATTCATCTCTTGGGCATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTCTCTCCAGAGGTCCCGTCCGACGGAGATGCCACCTCCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACACGGTACGGTCCGGCAGGGGAGAGCCACCTCAGGTGCATATTGAC	313
QY	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyralaGlyAsnAsp	80
DB	314	AACCGGGTACCGGGTGGCTGGCTGCTAAACCGCAGCACCATCTCTATCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle	100
DB	374	AAGTGTGCTGGATCTCTCGCTGGTCTTCTGAGCAACACCCAAACGACGATACAGCATC	433
QY	101	GluIleGlnAsnValAspValTyArgGlyProTyThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGACGGTGGATGTATGACGAGGGCCCTTACACCTGCTCGTGGCAGACAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACCAACCAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTTGAG	553
QY	141	IleSerSerAspIleSerIleAsnGlyAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTTCTCAGATATCTCATTATGAGGGACATATATGCTCCTACCTGCTGCTGCTGCTG	613
QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
DB	614	GGTAGCAGACGCTACGGTACTTGGAGACACATCTCCCAAGCGGTGGCTTTGTG	673
QY	181	SerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrglu	200
DB	674	AGTGAAGACGAATCTTGGAAATTCAGGCATCCCGGGAGCAGTCCAGGGACTACGAG	733
QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn	220
DB	734	TGCAGTGGCTCCTCAATGACGTGGCGCCGCGTGGTACGAGAGTAAAGTCACTGGAAC	793
QY	221	TyrProProTyIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
DB	794	TATCCACCATACATTTCCAGAACCAAGGTACAGGTGTCCTCCGGGACCAAGGGGACA	853
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyIleAspAspLys	260
DB	854	CTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGGTACAGGATGACAAA	913
QY	261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
DB	914	AGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTCTCTCAAAATCT	973
QY	281	IlePhePheAsnValSerGluHisAspTyrglyAsnTyThrCysValAlaSerAsnLys	300
DB	974	ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCTGCTGCTCAACAG	1033

QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
DB	1034	CTGGGCCACACCAATGCCAGCATCATGTATTGTGTCACGCGCCGCTCAGCGAGGTGAGC	1093
QY	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu	340
DB	1094	AACGGCAGCTCGAGGAGGCGAGTCCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1153
QY	341	LeuLeuLysPhe	344
DB	1154	CTTCTCAAAATTT	1165

RESULT 6

US-09-978-608A-522
 ; Sequence 522, Application US/09978608A
 ; Publication No. US20030045462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurhey, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C22
 ; CURRENT APPLICATION NUMBER: US/09/978,608A
 ; CURRENT FILING DATE: 2001-10-16
 ; NUMBER OF SEQ ID NOS: 624
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 522
 ; LENGTH: 1679
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-978-608A-522

Alignment Scores:
 Pred. No.: 9,94e-216 Length: 1679
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-608A-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCAACCCAGCCAAATTCATCTCTTGGGCATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40

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DB 194 GCTGCTGTGTCTTCTTCAAGGAGTGCCTGCGGAGGAGATGCGACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGACACAGTGCAGGTCGCGGAGGAGGAGGCGCCACCTCAGGTGCACATTGAC 313
QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACGGGTGCACCGGGTGCCTGCTAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrIleSerIle 100
DB 374 AAGTGGTGCCTGCATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
QY 101 GluIleGlnAsnValAspValThrAspGlnGlyGluSerValGlnThrAsp 120
DB 434 GAGATCCAGACGTCGATGATGACGAGGCGCTTACACCTGCTGCTGCTGCTGCTGCTG 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGTCCTCCTTGTGCAAGTATCTCCCAAAATGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGlnGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTTTCAGATATCTCCATTAATGAAGGAGCAATATTAGCTCCTCAGCTCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACAGAGCTACGCTTACTTGTGAGACACATCTCTCCCAAGCGGTGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyLeuThrArgGlnGlnSerGlyAspTyrGlu 200
DB 674 AGTAGAGAGCAATCTTGAATTCAGGCGCATCCCGGAGGAGGAGGAGGAGGAGGAGGAG 733
QY 201 CysSerAlaSerAsnAspValAlaLeuProValValArgValValValValValValVal 220
DB 734 TGCAAGTCCCAATGACGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 793
QY 221 TyrProProTyrIleSerGluAlaGlyGlyThrGlyValProValGlnGlyGlyThr 240
DB 794 TATCCACCATATCTTCAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnThrTyrLysAspAspLys 260
DB 854 CTGAGGTGAAGCTTCAGCAGTCCCTCAGCAGAAATCCAGTGTGACAGGAGTACAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrCysValAlaSerAsnLys 300
DB 974 ATCTTCTCAATGCTCTGAAACATGACTATGGAACTACACTTGGTGGGCTCCCAACAG 1033
QY 301 LeuGluHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320
DB 1034 CTGGGCGCACCAATGCCCATCATCTATTGTTGTCAGGCGCGCGCGCGCGCGCGCGCGCG 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValThrProLeuProLeuValLeuHisLeu 340
DB 1094 AACGGCACGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTCTCTCAAAATTT 1165
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RESULT 7

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US-09-978-585A-522
; Sequence 522, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Fillaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C15
CURRENT APPLICATION NUMBER: US/09/978.585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 522
LENGTH: 1679
TYPE: DNA
ORGANISM: Homo sapiens
US-09-978-585A-522
Alignment Scores:
Pred. No.: 9,948-216 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0
US-10-017-084A-523 (1-344) x US-09-978-585A-522 (1-1679)
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QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCAATCCAGCCAAAATGCACAATTTCTCTCTGGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAGGAGTGCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGACACAGTGCAGGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACGGGTGCACCGGGTGCCTGCTTAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrIleSerIle 100
DB 374 AAGTGGTGCCTGCATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
QY 101 GluIleGlnAsnValAspValThrAspGlnGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGACGTCGATGATGACGAGGCGCTTACACCTGCTGCTGCTGCTGCTGCTGCTG 493
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121 AsnHisProLysThrSerArgValHisLeuLeuValSerProLysIleValGlu 140
 Db 494 ACCACCAAGACCTTAGGTCCCTCATTTGTCAGATATCCCAAAATTTAGAG 553
 Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTTCTTCAGATATCCCAATTAAGAGGAACAATATTAGCCTCACCCTGATAGCACT 613
 Qy 161 GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACAGACGCTACGCTTACTTGGAGACACATCTCCCAAGCGGTTGGCTTTGG 673
 Qy 181 SerGluAspLysThrLeuGluIleGlnGlyIleThrArgGluGlnIleSerGlyAspTyrGlu 200
 Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGACTACGAG 733
 Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValLysValThrValAsn 220
 Db 734 TGCAGTCCCTCCCAATGACGTGGCGCCCTGGTACGAGAGTAAGGTCCACCGTGAC 793
 Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATACATTCAGAGCCAGGGGTACAGGTGTCCTCCGGGACAAAGGGGACA 853
 Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLysAspAspLys 260
 Db 854 CTGACGTGTGAGCCCTACGACGTCCCTCCAGCAGAAATCCAGTGTGATACAGGATGACAA 913
 Qy 261 ArgLeuIleGluLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTGAAGGAAGAAAGGGGTGAAAGTGGAAACAGACCTTCTCTCAAAACTC 973
 Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 Db 974 ATCTCTCTCAATGCTCTGCAACATGACTATGGGAACATACACTTGGCTCCCAACAAG 1033
 Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCGACACCAATGCCAGCATCATCTATTGTTGTCAGGGCGGTCAGGAGGTGAC 1093
 Qy 321 AsnGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu 340
 Db 1094 AAGCGCACGTCAGGAGGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
 Qy 341 LeuLeuLysPhe 344
 Db 1154 CTCTCAAAATTT 1165

RESULT 8

US-09-978-191A-522
 ; Sequence 522, Application US/09978191A

; Publication No. US20030050239A1
 ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hsien, Kenneth J.
 ; APPLICANT: K.Javin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C4
 ; CURRENT APPLICATION NUMBER: US/09/978,191A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9,94e-216	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-191A-522 (1-1679)

QY	1	MetLysThrIleGlnProValMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAACCATCCACCAAAATGCACATCTCTTGGGCACATCTTCACGGGCTG	193
QY	21	AlaAlaLeuCysLeupheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTGTGTCTCTTCCAGGAGTCCCGTCGCGAGGAGATGCCACCTTCCCCCAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGACACACGTGACGCTCCGCGAGGGAGAGCGCCACCTCAGTGCTACATATGAC	313
QY	61	AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80
DB	314	AACCGGTCAACCGGTGCTGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle	100
DB	374	AGTGTGCTGCTGATCTCTGCTGCTGCTCTTCTGAGCAACACCAACGACGACGACATC	433
QY	101	GluIleGlnAsnValAspValTyArgGluGlyProTyThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGAACGTGTATGACAGGGGCCCTTACACCTGCTGCTGTCAGACAGAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACACACCAAGACCTCTAGGGTCCACCTATTGTGCAAGATATCTCCAAATTTAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCTCATAGCAACT	613

QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACAGACCTACCGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTTGG 673
QY 181 SerGluAspGluLeuGluLeuGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGAGCAATCTTGAATTCAGGCGCATCCCGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAspValAlaAlaProValAlaArgValGlyValThrValAsn 220
DB 734 TGCAGTGCCTCAATGACGTGGCGCGCGGTACGAGAGTAAAGGTACCGTGAAC 793
QY 221 TyrProGluIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTCAGAAAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
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QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuProLeuValLeuHisLeu 340
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DB 1154 CTCTCTCAAAATTT 1165

RESULT 9
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Sequence 522, Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC17
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PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
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Alignment Scores:
Pred. No.: 9,94e-216 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

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DB 374 AAGTGTGCTGGATCCTCGCGTGGTCTTCTGAGCAACACCAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAAGCTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuValGlnValSerProLysIleValGlu 140
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DB 554 ATTTCTCAGATATCTCCATTAAAGAGGGAACATATTAGCCCTCACCTCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAAGACCTTACCTGTTGGACACATCTCTCCCAAGCGGTGGCTTTG 673
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 9,94e-216 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-564A-522 (1-1679)
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Alignment Scores:

Pred. No.: 9,94e-216 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-999-833A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCAAAATGCAAAATCTATCTCTTGGCAATCTTCACGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTGTGTCTCTTCCAGGAGTCCCGTCGGCAGGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrIleuArgCysThrIleAsp 60
DB 254 GCTATGACCAACGTGACGCTCCGCGAGGGAGAGGCCACCCAGGTGCACATTATGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleuTyrrAlaGlyAsnAsp 80
DB 314 AACCGGTTCACCGGGTGGCTGCGGTAAACCGCAGCACCATTCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrrSerile 100
DB 374 AAGTGGTCCCTGGATCCTCGGTGCTCTTCTGAGCAACCAACCAACACGATCAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrrAspGluGlyProTyrrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTCGTATGATGACGAGGGCCCTTACACCTGCTGCGTGCACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGTCCACCTCATTGTGCAAGTATCTCCCAAAATGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerIleuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTATGAGGGGAACAAATATTAGCTCACCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrrGlu 200
DB 674 AGTAGAGCAATACTTGGAAATTCAGGGCATCACCCTGGGAGCAGTACGGGGATACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValIleValThrValAsn 220
DB 734 TGCAGTGCCTCCAAATGACGTGCGCGCCCTGTGACGGAGAGTAAAGGTCAACGTGAAC 793
QY 221 TyrProTyrrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTTCAGAGCCAAAGGGTACAGGTGCCCTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrrTyrrLysAspLys 260
DB 854 CTGAGTGTGAGCCTCAGCAGTCCCTCCAGCAGAAATTCAGTGTGACAGATGACAA 913


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Alignment Scores:
Pred. No.: 9,94e-216 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-981-915A-522 (1-1679)
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTTPAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAAATTCATCTCTTGGCAATCTTACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGCCCGCGCAGCGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACACGTGACGGTCCGCGAGGGGAGAGCGCCCTCAGGTGCACTATTGAC 313
QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuThrAlaGlyAsnAsp 80
DB 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCCAGCACCATCTCTATGCTGGATGAC 373
QY 81 LysTPCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTCCCTGGATCTCGCGTGGTCTTCTGAGCAACACCCAGCGACAGCATC 433
QY 101 GluIleGlnAsnValaspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGACGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCACCCTCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTTPAlaGHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACACAGCGCTACGGTACTTGGACACACATCTCCCAAGCGGTTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCACTCAGGGGACTACAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValGlyValThrValAsn 220
DB 734 TGCAGTGCCCTCAATGACGTGGCGCGCGCGGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTTTCAGAGGCAAGGGGTACAGGTGTCCCGGTGGGCAAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnThrTyrLysAspAspLys 260
DB 854 CTGACGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTGAAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysValLysValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATGTAGGAAAGAAAGGGGTGAAGTGGAAAACACACACCTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaIleSerAsnLys 300
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Alignment Scores: 9.94e-216 1679.
 Pred. No.: 1806.00 344
 Score:

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 11 Indels: 0
 DB: 0 Gaps: 0
 US-10-017-084A-523 (1-344) x US-09-978-824-522 (1-1679)
 QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAARACCATCCAGCCAAAATGCACAATTCATCTCTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTGTGTCTCTTCCAAGGAGTCCCGTCGGCAGCGAGAGTCCACCTCCCAAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyLeuSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGACAACTGACGCTCCGACGGGGAGAGCGCCCTCAGGTGCTATTGTGAC 313
 QY 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGTCCACCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrIleTyrSerIle 100
 DB 374 AAGTGGTGGCTGGATCCCTCGGCTGGTCTTCTGAGCAACACCACCAACGATACGATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAAGCTGGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCCCAAGACCTCTAGGCTCCACCTCATTTGTCAAGTATCTCCCAAAATTTGATAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCCCTCATGACAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGAGCGCTACGGTACTTGGAGACACATCTCTCCCAAGCGGTGGCTGTG 673
 QY 181 SerGluAspGluTyrIleGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCAGGAGCAGTACAGGGGACTAGG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
 DB -734 TGCAGTGCCTCCAATGACGTGGCGCGCGCTGGTACGGAGAGTAAAGGTACCGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValIleGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTCAAGAGCCAAAGGGTACAGGTGTCCCGTGGGACAAAAGGG 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAGAATTCACGTGTGTCAGAGATGACAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTTGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACACTTTCCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCATGTCTCTGAACATGACTATGGGAACACTACATCTGGTGGCTCCACAGAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACCAATGCCAGCATCATCTATTGGTCCAGCGCGCGTCCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340

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Alignment Scores:

Pred. No.: 9,94e-216 Length: 1679
 Score: 1806.00 Matches: 344
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-918-585A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCCAAAAATGCACAAATCTATCTCTTGGCAATCTTTCACGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAAAGGAGTCCCGTGCAGCGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGACACGTCAGCGTCCGGCAGGGGAGAGCCACCTCAGGTGCACATTGAC 313
 QY 61 AsnArgValThrArgValAlaIleValLeuAsnArgSerThrIleLeuValAlaGlyAsnAsp 80
 DB 314 ACCGGGTCCACCGGGTGGCTGGCTAAACCCGACGACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrIleSerIle 100
 DB 374 AGCTGGTGGTGGATCTCGCTGGTCTCTTGGACACACCCAAACGACGACGATC 433
 QY 101 GluIleGlnAsnValAspValThrAspGluGlyProThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGACGTTGGATGTATGACGAGGGCCCTTACCTCTCGGTGCAGACAGC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 ACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTCAGATATCTCCATTAATGAAGGGAACAATATAGCTCAGCTCATAGCACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGCGCTACGCTTACTTGGACACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluThrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
 DB 674 AGTGAAGACGAAATCTTGGAAATTCAGGGGCATCCCGGGAGCAGTCAGGGAGTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValAlaArgValValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCCCAATGACGTGGCGCCGCCGCTGGTACGGAGGTAAAGGTACCGTGAAC 793
 QY 221 TyrProProThrIleSerGluAlaLysGlyThrGlyValProValGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTTCAGAACGAGGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 DB 854 CTGACGTGTAAGGCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTACAAAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAAGAGGGGTGAAAGTGGAAACAGACACCTTTCTCTCAAAACTC 973
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 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGCCACACCCATGCCGACATGCTATTTGGTCCAGGCGCGCTCAGGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuLeuHisLeu 340
 DB 1094 AACGGCAGCTCAGGAGGGGAGGGTGGCTGCTGCTGCTCTTCTGCTCTTGGTCTTGGCACCTG 1153
 QY 341 LeuLeuLysPhe 344
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RESULT 15

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC21
; CURRENT APPLICATION NUMBER: US/09/978,423A
; CURRENT FILING DATE: 2002-05-16
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51	PRIOR APPLICATION NUMBER: 60/085573
52	PRIOR FILING DATE: 1998-05-15
53	PRIOR APPLICATION NUMBER: 60/085704
54	PRIOR FILING DATE: 1998-05-15
55	PRIOR APPLICATION NUMBER: 60/085697

US-10-017-084A-523 (1-344) x US-09-978-423A-522 (1-1679)

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Db	134	ATGAAACCAATCAGCCAAAATGCAAATTCATCTCTGGCAATCTTCACGGGGCTG	193
Q7	21	AlaAlaLeuCysLeuPheGlnIleValProValArgSerGlyAspAlaThrPheProLys	40
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Db	194	GCTGCTGTGTCTCTTCCAGAGAGTCCCGTCGCGACGGAGATGCCACCTCCCAAA	253

Qy	41	AlaMetAspAsnValThrValArgGlnGlySerAlaThrLeuArgCysThrIleasp	60
Db	254	GCTATGACACGTGACGGTCCGGCAGGGGAGAGCGCACCCCTCAGGTGCTATTGAC	313
Qy	61	AsnArgValThrArgValAlaTatLeuAsnArgSerThrIleLeuTyralaGlyAsnAsp	80
Db	314	AACCGGGTCACCGGGTGGCTGGCTAAACCCGACACCATCTCTATGCTCGGGAAATGAC	373
Qy	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle	100
Db	374	AAGTGGTGGCTCGGATCCCTCGCGTGGTCTCTTCAGACAACACCAACAGCAGTACAGCATC	433
Qy	101	GluIleGlnAsnValAspValTyArgSpGluGlyProTyThrCysSerValGlnThrAsp	120
Db	434	GAGATCCAGAACGTCGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACGACACAC	493
Qy	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
Db	494	AAACCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTCTAGAC	553
Qy	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
Db	554	ATTTCTTCAGATATCTCCATTTATGAGGAGCAATATATAGCTCCTACCTGCATACCACT	613
Qy	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysIleValGlyPheVal	180
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Qy	181	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrglu	200
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Qy	201	CysSerAlaSerAsnAspValAlaAlaProValAlaArgValLysValThrValAsn	220
Db	734	TGCAGTGCCTCCAATGACGTGGCGGGCCGGTGGTACCGGAGAGTAAGGTCCACCGTGAAC	793
Qy	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
Db	794	TATCCACCATCATTTTCAGAAAGCAAGGTCACAGGTGTCCCGGTGGGACAAAGGGGACA	853
Qy	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrllysAspLys	260
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACAGTGGTACAAGGATCACAAA	913
Qy	261	ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
Db	914	AGACTGATGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTTCCTCTCAAAACCTC	973
Qy	281	IlePhePheAsnValSerGluHisAspTyrglyAsnTyrrhrCysValAlaSerAsnLys	300
Db	974	ATCTCTTCATGTCTCTGAACATGACTATGGGAACACTACCTTCGCTGGCTCCACNANG	1033
Qy	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValser	320
Db	1034	CTGGGCCACACCAATGCCAGCATCAATGCTATTGTGTCAGGCGCCCTCAGCAGGTGAGC	1093
Qy	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu	340
Db	1094	AACGGCACGCTCGAGGAGGGCAGGCTCGTGGCTGTGCTCTTCTGTGCTTCGTGACCTG	1153
Qy	341	LeuLeuLysPhe	344
Db	1154	CTTCTCAAAATTT	1165

Search completed: September 11, 2003, 05:38:57
Job time : 1482 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2003, 03:07:39 ; Search time 2500 Seconds
(without alignments)
3344.296 Million cell updates/sec

Title: US-10-017-084A-523
Per-fect score: 1806
Sequence: 1 MKTIQPKHNSISWAFTGL.....RRAGCVWLLPLVLLHLLKF 344

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPTO.spool_p/US10017084/runat_09092003_141326_21883/app.query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-USER=US10017084.cgn_1.1.3549 -runat_09092003_141326_21883 -NCPU=6 -ICPU=3
-NO_XMAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
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5: em_estpl.*
6: em_estro.*
7: em_htc.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
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20: em_gss_vrt.*
21: em_gss_fun.*
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23: em_gss_mus.*
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27: em_gss_vrl.*
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29: gb_gss2.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1780	98.6	1808	11	AK045973 Mus muscu
2	1780	98.6	1808	11	AK046377 Mus muscu
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4	1199.5	66.4	856	13	BU155617 AGENCOURT
5	1167	64.6	1039	10	BE798585 601581610
6	1112	61.6	890	14	CD327172 AGENCOURT
7	1062.5	58.8	1085	9	AL533026 AL533026
8	1047	58.0	740	13	BU368328 603789424
9	1042	57.7	840	13	BU320256 603851118
10	1005.5	55.7	849	13	BU755360 603024964
11	982.5	54.4	865	12	BI666583 603291469
12	973	53.9	601	14	CB582386 AMGNNUC-N
13	929	51.4	793	13	BU365385 603786031
14	926	51.3	545	10	BE263639 601192064
15	925.5	51.2	979	10	BG261691 602373361
16	916.5	50.7	2768	11	AK030681 Mus muscu
17	912	50.5	732	12	BI551784 603197479
18	910	50.4	553	10	BE864555 UI-M-BH1-
19	907	50.2	524	10	BE014142 AGENCOURT
20	902.5	50.0	859	14	CD325278 AGENCOURT
21	894	49.5	2467	11	AK044845 Mus muscu
22	890	49.3	784	12	BI549918 AGENCOURT
23	881	48.8	768	9	AU080629 AU080629
24	875	48.4	754	12	BI550038 603182302
25	869	47.8	1580	12	BI548586 603189502
26	865.5	47.8	891	12	BM003450 603629962
27	862.5	47.8	953	12	BM423716 AGENCOURT
28	858.5	47.5	1033	12	BM807426 AGENCOURT
29	853.5	47.4	1083	12	BM805227 AGENCOURT
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31	818	45.1	1138	14	CD335354 UI-M-GMO-
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33	811.5	44.6	2096	11	BM256660 520043 MA
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35	801	44.2	1953	11	BG704152 602687364
36	799	44.2	1953	11	AK030503 Mus muscu
37	795	44.0	660	14	BY723873 BY723873
38	791.5	43.8	764	12	BM945665 UI-M-EMO-
39	772.5	42.8	849	14	CA472810 AGENCOURT
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41	770	42.6	671	10	BB644996 BB644996
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44	759	42.0	2534	11	AK039193 Mus muscu
45	742	41.1	827	14	CA306798 UI-H-FH1-

ALIGNMENTS

RESULT 1
AK045973
LOCUS
DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN
full-length enriched library, clone:B230328N06 product:NEUROTRIMIN
PRECUSOR (cp65) homolog (Rattus norvegicus), full insert sequence.
ACCESSION AK045973
VERSION AK045973.1 GI:26337738
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
PUBMED
REFERENCE
AUTHORS

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Quackenbush, J., Schriml, L.M., Staib, J., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, I., Kawai, J., Kontsuki, S.,
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

TITLE
JOURNAL
MEDLINE
PUBMED
PUBMED
REFERENCE
AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1808)
Fukuda, S., Furuno, M., Hayashizaki, Y., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kihara, C., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome

TITLE
JOURNAL
MEDLINE
PUBMED
PUBMED
REFERENCE
AUTHORS

7 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
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Nature 420, 563-573 (2002)
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Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome

COMMENT

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/

FEATURES

Location/Qualifiers

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ORIGIN

CDS

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Best Local Similarity: 97.97% Mismatches: 2
Query Match: 98.56% Indels: 0
DB: 11 Gaps: 0
US-10-017-084A-523 (1-344) x AK045973 (1-1808)

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DEFINITION	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230377K17 product:NEUROTRIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.		
ACCESSION	AK046377		
VERSION	1	GI:26338018	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Euteleostomi; Carninci, P. and Hayashizaki, Y.		
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)		
JOURNAL	99279253		
MEDLINE	10349636		
PUBMED			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		

Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

source

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BASE COUNT 550 a 431 c 462 g 365 t

ORIGIN

Alignment Scores:
Pred. No.: 1,73e-192 Length: 1808
Score: 1780.00 Matches: 337
Percent Similarity: 99.42% Conservative: 5
Best Local Similarity: 97.97% Mismatches: 2
Query Match: 98.56% Indels: 0
DB: 11 Gaps: 0

US-10-017-084a-523 (1-344) x AK046377 (1-1808)

OY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrClyLeu 20
DB 204 ATGAATAACCATCCAGGCAAAATGACAAATCTATCTCTGCGGCATCTTCACGGGCTG 263
OY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys 40
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VERSION CD354474.1 GI:31146975
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5
Location/Qualifiers
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source

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ACCESSION BE798585
 VERSION BE798585.1 GI:10219783

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 1039)

NIH-MGC http://mgs.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: DCDT/PTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LICM779 row: d column: 04
 High quality sequence stop: 849.

Location/Qualifiers

FEATURES

source

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 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 274 a 271 c 286 g 207 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 115e-122 Length: 1039
 Score: 1167.00 Matches: 243
 Percent Similarity: 80.71% Conservatives: 8
 Best Local Similarity: 78.14% Mismatches: 24
 Query Match: 64.62% Indels: 37
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 US-10-017-084A-523 (1-344) x BE798585 (1-1039)

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ACCESSION AL533026
 VERSION AL533026.2 GI:31070858
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1085)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 13, 2001 this sequence version replaced gi:12796519.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6387.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DN005DB100P1cluster=6387.f. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DN005DB100P1.
 Location/Qualifiers
 1. 1085
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DN005YD20"
 /tissue.type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_lib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 BASE COUNT 318 a 261 c 263 g 234 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1136-110 Length: 1085
 Score: 1062.50 Matches: 211
 Percent Similarity: 84.18% Conservative: 2
 Best Local Similarity: 83.40% Mismatches: 0
 Query Match: 58.83% Indels: 40
 Gaps: 1
 DB: 1
 US-10-017-084A-523 (1-344) x AL533026 (1-1085)
 QY 132 ValGlnValSerProTylsileValGluileSerSerAspIleSerIleAsnGluGlyAsn 151
 Db 156 ATTAAGATATCTCCCAAAATGTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 215
 QY 152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
 Db 216 AATATTAGCTTACCTGCATAGCAACTGGTAGACAGACCTACGGTTACTTGGAGACAC 275
 QY 172 IleSerProTylsAlaValGlyPheValSerGluAspLutyrLeuGluileGlnGlyIle 191
 Db 276 ATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAATCTTGAATTCAGGCGATC 335
 QY 192 ThrArgGluClnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
 Db 336 ACCGGGAGGCGTACAGGAGTACAGTGCAGTGCCTCCATGAGTGGCGCGCCCGG 395
 QY 212 ValArgArgVallysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231
 Db 396 GTAGGGAGATAAGCTCACCGTGAACATATCCACCATACTTTCAGAGCGAAGGAGTACA 455
 QY 232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
 Db 455
 456 GGTGTCCTCCCGTGGGACAAAAGGGACACTCCAGTGTGAAGCCTCAGCAGTCCCTCAGCA 515
 QY 252 GlupheGlnTrpTyrLysAspLys 260
 Db 516 GAATTCAGTGTAGACAGGATGACAAAAGAGCTGAAAATCTCATTACAGTTTGGTTATGA 575
 QY 260 260
 Db 576 TGGGAAAGCTTCTCCCATCGTGGACGAATGTGTCAAAACGGCCAGTGGGATCAATCA 635
 QY 261 261
 Db 636 GCCTGACTTCTCGCAGCAATCTCCCGACTGATGAAGGAAAAGGGGTGAAGGTGA 695
 QY 272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292
 Db 696 AACAGACCTTCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGAA 755
 QY 292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheG 312
 Db 756 CTACACTTCGCTGGCTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATT 815
 QY 312 yProGlyAlaValSerGluValSerAsnGlyThrSerArgAlaGlyCysValTrpLe 332
 Db 816 TCAGAGCGCGTCAGCGAGGTGACCAAGCGACGTGAGGAGGCGAGCTCGCTCGCTG 875
 QY 332 uLeuProLeuLeuValLeuHisLeuLeuLysPhe 344
 Db 876 GCTGCTCTTCTGGTCTTGCACCTGCTTCTCAAAATTT 912
 RESULT 8
 BU368328
 LOCUS
 DEFINITION 740 bp mRNA linear EST 28-NOV-2002
 603789424F1 CSEQCHN72 Gallus gallus cDNA clone ChEST750p6 5', mRNA
 sequence.
 ACCESSION BU368328
 VERSION BU368328.1 GI:25876329
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus
 1. (bases 1 to 740)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.P., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 MEDLINE
 PUBMED 12445392
 COMMENT
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 10D, UK
 Tel: 0161208930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1. 740
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="ChEST750p6"
 /sex="Female"
 /tissue_type="cerebrum"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN72"
 /note="Organ: brain; Vector: pBluescript II KS(+); Site: 1.
 EcoRI; Site: 2. NotI; This normalized library was
 constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom-modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 170 a 234 c 207 g 129 t
ORIGIN
Alignment Scores:
Pred. No.: 3.8e-109 Length: 740
Score: 1047.00 Matches: 192
Percent Similarity: 91.8% Conservative: 22
Best Local Similarity: 82.4% Mismatches: 19
Query Match: 57.9% Indels: 0
DB: 13 Gaps: 0

US-10-017-084A-523 (1-344) x BU368328 (1-740)

QY 101 GlnUleGlnValaspValtyrAspGluGlyProtyrThrCysSerValGlnThrAsp 120
DB 3 CAGATCCAGCGTGGAGCTGATGATGAGGCGCCCTACACCTGCTCGTGACAGACAG 62
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 63 AATCACCACCAAGACATCTCGCTGCACCTCATTTGTGCAAGTGTCCGCGAAATTAACGAG 122
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 123 ATCTCTCTGACATCTCCATCAATGAAGGTGGCAAGTCAGCTCAGCTCAGTACGACG 182
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 183 GGCAGGCCAGACCCACCAATCACCTGGAGACACATCTGCCCAAGGTGGGCTTCATC 242
QY 181 SerGlnAspGluThrLeuGluIleGlnGlyLeuThrArgGlnGlnSerGlyAspThrGlu 200
DB 243 AGCAGGACGAGTACTGGAGATCACAGGCTCAGGAGGAGGAGTGGCGGAGTACGAG 302
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
DB 303 TGCAGTGCCTCAGACGCTGGCCGCCCTGTCTGTCAGGAGTCAAGTCAACGCTCAAC 362
QY 221 TyrProProtyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 363 TACCCACCTGATCTCGGATGCGAGAGACCGGTGTCCCGGTGGGCGAGAGGCGATC 422
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
DB 423 CTGATGTGTGAAGCTCGCTGCTGCCCTCCAGTCCAGTCCAGTCAAGAGACGACAG 482
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 483 CGCTGCTGAGGACAGAAAGGCTGAAGTGGAAACAAAGCTCTCTCCGACTG 542
QY 281 IlePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
DB 543 ACTTCTTCACTCTCCGACGAGGACTACGCACTGCTGGGCTGCTCCACACG 602
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 603 CTAGGAACACCAAGCCAGCATGATCTTTATGGCCCGGTGGCGTGCAGTGCAGTGCAC 662
QY 321 AsnGlyThrSerArgArgAlaClyCysValTrpLeu 333
DB 663 AGCGGTGCGTGGCGGAGGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 701

RESULT 9

BU320256 840 bp mRNA linear EST 28-NOV-2002
LOCUS 603851118F1 CSEQCHN62 Gallus gallus CDNA clone CHEST847d5 5', mRNA
DEFINITION sequence.
ACCESSION BU320256
VERSION BU320256.1 GI:25828257
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
REFERENCE 1 (bases 1 to 840)
AUTHORS Boardman, P.E.; Sanz-Ezquerro, J.; Overton, I.M.; Burt, D.W.; Bosch, E.;
Fong, W.T.; Tickle, C.; Brown, W.R.A.; Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curri Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)

PO Box 88, Manchester, M60 1OD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk

FEATURES
Location/Qualifiers
source 1..840

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, HiseX"
/db_xref="taxon:9031"
/clone="CHEST847d5"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQCHN62"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
ECORI. Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

BASE COUNT 210 a 256 c 231 g 143 t
ORIGIN
Alignment Scores:
Pred. No.: 1.71e-108 Length: 840
Score: 1042.00 Matches: 194
Percent Similarity: 91.14% Conservative: 22
Best Local Similarity: 81.86% Mismatches: 20
Query Match: 57.70% Indels: 1
DB: 13 Gaps: 0
US-10-017-084A-523 (1-344) x BU320256 (1-840)

QY 98 TyrSerIleGluIleGlnAsnValaspValtyrAspGluGlyProtyrThrCysSerVal 117
DB 2 TACAGATCCAGTCCAGCGTGGAGCTGATGATGAGGCGCCCTACACCTGCTCGTG 61
QY 118 GlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLys 137
DB 62 CAGACAGACAAATCACCCCAAGACATCTCGCTGCACCTCATTTGTGCAAGTGTCCGCGAA 121
QY 138 IleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCys 157

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122 ATTACCGAGATCTTCTGACATCTCCATCAATGAAGTGGCAAGCTCAGCCTCACCTGC 181
158 ILeAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaVal 177
182 ATAGCCACGGGAGGAGCCACCAATCACTGAGACATCTGCCCAAGCTGTG 241
178 GlyPheValSerGluAspGluLeuIleGlnGlyThrArgGluGlnSerGly 197
242 GGCTTCATCAGGAGGAGGAGTACTGAGATCAGAGCATCAGAGGGAGGAGTGGGC 301
198 AspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgValLysVal 217
302 GAGTACGAGTGCAGTGCCTCCACAGCTGGCCGCCCTGCTCCAGCGAGTCAAGTGC 361
218 ThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGln 237
362 ACCGTCAACTACCCACCGTACATCTCGATGCGAAGAGCAGCGGTGGCGGAG 421
238 LysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLys 257
422 AAGGGCATCTGATGTGTAAGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
258 AspAspLysArgLeuIleGluGlyLysGlyValLysValLysValLysValLysVal 277
482 GACGACAGCGGTGGCTGTAAGGAGCAGAAAGGCTGAAGGTGGAAACAAAGGCTTCTTC 541
278 SerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAla 297
542 TCCGAGCTGACTTCTTCAAGCTCTCCGAGCAGGACTACGGCAACTACACCTGCGTGGCC 601
298 SerAsnLysLeuGluHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSer 317
602 TCCACACGCTAAACAAACCAACGAGCAGCATGATCTTTATGGCCCGGTGGAGTGCAC 661
318 GluValSerAsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeu 333
662 GATGGCAACAGCGGTGGCTGGCGGAGGAGCAGCTGTGCTGGCTGGCTGGCTGG 710

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RESULT 10
5-753360
LOCUS 603024964F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195750 5',
DEFINITION mRNA sequence.
ACCESSION BI7553360
VERSION BI7553360.1 GI:15746938
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 849)
NIH-MGC http://imgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: rcp@bbs.fda.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11489 row: o column: 15
High quality sequence stop: 848.
Location/Qualifiers
1. 849
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5195750"
/lab_host="DH10B"

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FEATURES

source

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/clone_lib="NIH_MGC_114"
/Note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
BASE COUNT 218 a 239 c 227 g 165 t
ORIGIN
Alignment Scores:
Pred. No.: 2,63e-104 Length: 849
Score: 1005.50 Matches: 190
Percent Similarity: 86.11% Conservative: 27
Best Local Similarity: 75.40% Mismatches: 33
Query Match: 55.68% Indels: 2
DB: 12 Gaps: 1
US-10-017-084A-523 (1-344) x BI7553360 (1-849)
QY 7 LysMetHisAsnSerIleSerTyrAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe 26
DB 83 GAGATGATACCATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 142
QY 27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46
DB 143 CCAGGAGTCCCTGCGCAGCGGAGATGCCACCTTCCCAAGAGCTATGGACACGTCG 202
QY 47 ValArgGlnGlyCysSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66
DB 203 GTCGCGCAGGCGGAGCGCCACCTTCAGCTGTACCATAGATGACCGGGTAACCGGGTG 262
QY 67 AlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTyrCysLeuAspPro 86
DB 263 GCCTGGCTAAACCGGAGCAGCATCTCTACGCTGGGAAGAGCAAGTGGTCCATAGACCT 322
QY 87 ArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAsp 106
DB 323 CGTGTGATCATCTGCTCAATACACCAACCCAGTACAGATCATGATCCAAATGTGGAT 382
QY 107 ValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSer 126
DB 383 GTGTATGACGAAGGTCCTACACCTGCTGTGTCAGACAGACAATCATCCCAAAACGTC 442
QY 127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146
DB 443 CGGTTTCACCTTAATAGTCAAGTTCCTCCTCAGATCATGAATATCTCTCAGACATCAT 502
QY 147 IleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166
DB 503 GTGAATGAGGAAGCAGTGTGACCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
QY 167 ValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyr 185
DB 563 GTGACATGGAGACACCTGTGCTCAGTCAACGAGGCGGCTTTGTAAGTGAGGATGAGTAC 622
QY 186 LeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsn 205
DB 623 CTGGAGATCTCTGACATCAACGAGACCATCTCGGGGAGTACGTAAGTCCAGCGCTTCA 682
QY 206 AspValAlaAlaProValValArgValLysValThrValAsnTyrProProTyrIle 225
DB 683 GATGTGCTGCGCGCGAGTGTGCGGAAAGTCAAAATCTGCTCAACTATCTCCCTATAT 742
QY 225 eSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAl 245
DB 743 CTCAAAAGCAAGCAACTGTGTGTTTTCAGTCCGCGCAGAGGAGGAGGAGGAGGAGG 802
QY 245 aSerAlaValProSerAlaGluPheGlnTyrTyr 256

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DB      803 CTCGAGTCCCATGGCTGAATCCAGTGGTTC 836
RESULT 11
LOCUS   BI666583
DEFINITION
503291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',
mRNA sequence.
ACCESSION BI666583
VERSION   BI666583.1 GI:15580816
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 865)
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NIH-MGC http://mgi.nci.nih.gov/
JOURNAL   National Institutes Of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11787 row: j column: 18
High quality sequence stop: 742.
FEATURES
     source
     1. 865
     Location/Qualifiers
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         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="IMAGE:5310833"
         /tissue_type="hypothalamus"
         /lab_host="DH10B"
         /clone_lib="NIH_MGC_96"
         /note="Organ: Brain; Vector: pBluescriptR (modified
         pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcggg
         ); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTVN-3',
         size-selected for average insert size 2.3 kb and
         normalized to ROT 5. This is a primary library enriched
         for full-length clones and constructed using the
         Cap-trapper method (Carninci, in preparation). Library
         constructed by M. Brownstein (NIH/NHGRI, National
         Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 250 a 230 c 209 g 176 t
ORIGIN
Alignment Scores:
Pred. No.: 1.16e-101 Length: 865
Score: 982.50 Matches: 207
Percent Similarity: 90.91% Conservative: 3
Best Local Similarity: 89.61% Mismatches: 13
Query Match: 54.40% Indels: 8
DB: 12 Gaps: 3

US-10-017-084A-523 (1-344) x BI666583 (1-865)
QY      1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB      183 ATGAACAACATCCAGCCCAAAATGCAATCTATCTCTGGGCAATCTTCACGGGGGTG 242
QY      21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB      243 GCTGCTCTGTGCTCTTCCAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAA 302
QY      41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB      303 GCTATGGACACAGTGGACGGTCCGGCAGGGGAGACGCCACCTCAGGTGCACATTATGAC 362

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QY      61 AsnArgValThrArgValAlaValTrrPLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB      363 AACCGGGTCACCGGGTGGCTGCTAAACCCGACGACCATCTCTATGCTGGGAATGAC 422
QY      81 LysTrpCysLeuAspProArgValValLeuLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB      423 AAGTGTGCTGCTGATCTCGCTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 482
QY      101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB      483 GAGATCCAGACGCTGATGTGTATGACGAGGGCCCTTACACTGCTCGTGCAGACAGAC 542
QY      121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB      543 AACACCCCAAGACCTCTAGGGTCCACCTCATTTGGCAAGTATCTCCCAAAATTTGAGAG 602
QY      141 IleSerSerAspIleSerIleAsnGluGlyAsn-AsnIleSerLeuThrCysIleAlaTh 160
DB      603 ATTCTTCAGATATCTCCATTATGAGGGAACAATATTAGCTCACCCTGATAGCAAC 662
QY      160 rGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVa 180
DB      663 TGTAGACACGAGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTGT 722
QY      180 lSerGluAspGluTyrLeu---GluIleGlnGlyIleThrArgGlu-GlnSer---GlyA 198
DB      723 GAGTGAAGACGAACTACTTTGGGAACCTTCAGGGCCATCTCCGGGGAGCCAGTCAAGGG 782
QY      198 sPtyrGluCys-SerAlaSerAsn-AspValAlaAla-ProValValArgArgValLysV 217
DB      783 TAACGAGTTGGCAGTGCCTCAATGGACGTTGGCGCGCCCTGGTGTACGGAGAAGTACAC 842
QY      217 alThrValAsnTyr---ProPro 223
DB      -843 AGTCCACGGATATTTTCCACCA 865

RESULT 12
LOCUS   CB582386
DEFINITION
AMGNNUC:NRHYS-00414-H5-A W Rat hypothalamus (10471) Rattus
norvegicus cDNA clone nrhys-00414-h5 5', mRNA sequence.
ACCESSION CB582386
VERSION   CB582386.1 GI:29526427
KEYWORDS  EST.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 601)
AUTHORS  Angen EST Program.
TITLE     Angen Rat EST Program
JOURNAL   Unpublished
COMMENT   Contact: Dan Fitzpatrick
Angen, Inc.
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805.447-4881
Plate: 00414; row: h column: 5.
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     1. 601
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     /db_xref="taxon:10116"
     /clone="nrhys-00414-h5"
     /clone_lib="W Rat hypothalamus (10471)"
     /note="Vector: pSPOR1; Site:1: SalI; Site:2: NotI; W Rat
     hypothalamus adult female Wistar rat avg. insert size 2.3
     kb fraction 6 and 7"
BASE COUNT 151 a 157 c 162 g 130 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 8.25e-101 Length: 601

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Score: 973.00 Matches: 182
 Percent Similarity: 98.95% Conservative: 6
 Best Local Similarity: 95.79% Mismatches: 2
 Query Match: 53.88% Indels: 0
 DB: 14 Gaps: 0

US-10-017-084A-523 (1-344) x CB582386 (1-601)

QY 155 LeuThrCysLeuAlaThrGlyArgProGluProThrValThrTrpArgHisSerPro 174
 DB 15 CTCAGTGCATGCCACAGGTAGACCGGAGCCCTACAGTAACCTGGAGACATATTTCTCC 74
 QY 175 LysAlaValGlyPheValSerGluAspGluThrLeuGlyGlyThrArgGlu 194
 DB 75 AAACCTGCTGGCTTGTGAGTGAGTGAAGTACTGAGATCCAGGGGCTACCTGGAG 134
 QY 195 GlnSerGlyAspThrGluCysSerAlaSerAsnAspValAlaAlaProValValArg 214
 DB 135 CAGTCAGCGAGTATGATGTCAGGCGCTCCAGCAGCTGGCAGCAGCAGTCTGACGAGA 194
 QY 215 ValLysValThrValAsnThrProProThrLysSerGluAlaLysGlyThrGlyValPro 234
 DB 195 GTGAAGTCCAGCTGAACATATCCACCATATCTCAGAAAGCTTAAGGGTACAGGTGTC 254
 QY 235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
 DB 255 GTGGGGCAGAGGGGACTCTGCAGTGTGAAGCCTCGCAGTCCCTTCAGCAGAAATTT 314
 QY 255 TrpThrLysAspLysArgLeuLeuGluGlyLysGlyValLysValGluAsnArg 274
 DB 315 TGGTTCAGGATGACAAAGACTGGTTGAAGGGAAGAGGAGTCAAGTGGAAACAGA 374
 QY 275 ProPheLeuSerLysLeuPhePheAsnValSerGluHisAspThrGlyAsnThr 294
 DB 375 CTTTTCCTTCAAGACTACCTTTTTTCAACGCTCTGTGAACAGCATATGGGAACATCA 434
 QY 295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGly 314
 DB 435 TGTGTGCATCCAAAGTGGGCCACACCAATGCCAGCATATGCTATTTGGCCAGGT 494
 QY 315 AlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValThrLeuPro 334
 DB 495 GCTGTGACGAGGTCAACATGGAGCTCAGGAGGCGANGCTGATTTGGCTCTCCCT 554
 QY 335 LeuLeuValLeuHisLeuLeuLysPhe 344
 DB 555 CTTCTGTCTTACACTGCTCTCAAAATTT 584

RESULT 13
 BU365385

LOCUS 603786031F1 CSBQCHN72 Gallus gallus linear EST 28-NOV-2002
 DEFINITION 793 bp mRNA clone ChEST742m7 5', mRNA

ACCESSION BU365385

VERSION BU365385.1 GI:25873373

KEYWORDS EST

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

BOARDMAN, P. F., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,

Fong, W. T., Tickle, C., Brown, W. A., Wilson, S. A., and Hubbard, S. J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

22355334

12445392

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FEATURES
 Location/Qualifiers

1..793
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="caon:9031"
 /clone="ChEST742m7"
 /sex="Female"
 /tissue_type="cerebrum"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN72"

/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

BASE COUNT 194 a 230 c 231 g 138 t

ORIGIN

Alignment Scores:
 Pred. No.: 1368-95 Length: 793
 Score: 929.00 Matches: 172
 Percent Similarity: 91.43% Conservative: 20
 Best Local Similarity: 81.90% Mismatches: 18
 Query Match: 51.44% Indels: 0
 DB: 13 Gaps: 0

US-10-017-084A-523 (1-344) x BU365385 (1-793)

QY 124 LysThrSerArgValHisLeuLeuValGlnValSerProLysLeuValGluLeuSerSer 143
 DB 1 AAGACATCTCGCGTGCACCTCATTTGTCAGAGTCTCCGCAAAATTTACCGAGATCTCTCT 60
 QY 144 AspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgPro 163
 DB 61 GACATCTCCATCAATGAAGGTGGCAGAGTGCAGCTCACCCTGCATAGCCAGCGGAGGCCA 120
 QY 164 GluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAsp 183
 DB 121 GACCCCAACATCACCTGGAGACACATCTCGCCCAAGCTGTGGGCTTCATCAGCAGGAC 180
 QY 184 GluThrLeuGluLeuGlnGlyThrArgGluGlnSerGlyAspThrGlyCysSerAla 203
 DB 181 GAGTACTCGAGATCACAGGCATCACGAGGAGCAGTGGCGAGTACGAGTACGAGTGC 240
 QY 204 SerAsnAspValAlaAlaProValValArgValLysValThrValAsnThrProPro 223
 DB 241 TCCACGAGGTGGCGCGCTGTGCTCCAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 300
 QY 224 TyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCys 243
 DB 301 TACATCTCGATCGAAGACACCGCGTGTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 QY 244 GluAlaSerAlaValProSerAlaGluPheGlnThrTrpThrLysAspLysArgLeuLeu 263
 DB 361 GAAGCCTCCGCTGTCCCTCGCTGACTTCCAGTGGTACAAAGACGACAAAGCGGCTGGCT 420
 QY 264 GluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeuLeuPhePhe 283
 DB 421 GAAGGACAGAAAGGCTGAAGGTGAAACAAAGAGGCTTCTTCTCCGACTGACTTCTTCTTC 480

ORIGIN

Alignment Scores: 4.69e-95 Length: 979
 Pred. No.: 925.50 Matches: 207
 Score: 87.70% Conservative: 7
 Best Similarity: 84.84% Mismatches: 26
 Query Match: 51.25% Indels: 11
 DS: 10 Gaps: 2

US-10-017-084A-523 (1-344) x BG261691 (1-979)

```

QY 12 IleserTrrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe-----GlnGly 28
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 CTGCCCTGGAGAGTGCCTCGTGTCTCTCAGGCTGCTATTCTTGTACCCACAGGA 126
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 GTGCCGGTGGTAGGGAGATGCCACCTTCCCAAAGCTATGCACAACGTGACGGTCAGG 186
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrrp 68
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 CAGGGGAGAGCGCCACCCTCAGGTGCACAAATTGACACCGAGTCACCCGGGTGGCTGG 246
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 LeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 CTAACCGCAGTACCATCTCTATGCTGGAAATGACAGAGTGGTCTAGATCCCTCGGTGG 306
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 307 GTCTCTCTGAGTAACACCCAGCAGCCAGTACAGATTTGAGATCCAGATGTGGATGTGAC 366
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 109 AspGlnGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 367 GATGAGGGCCCTTATACCTGCTCGGTACAGACAGACACACCCCTTAAGACCTCCAGGTC- 425
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 426 CACCTCATTTGTACAAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCATTAA 485
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 486 GAGGGAACAACATCAGCCTCATTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACC 545
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIle 188
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 546 TGGAGACATATTCTCCCAAGCGCTTGGCTTTGTGAGTGGATGAGTCTCTGGAGATC 605
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 GlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAla 208
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 506 CAGGACATCACTCGGGNACATCAGCGGAGTACGAGTGCAGCGCTC--AACGACGTGGCG 663
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 209 AlaProValValArgValLysValThrValAsnTyrProProTyrIleSerGluAla 228
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 664 G--ACCGTGTAGAGAGTGAAGGTCCC--GTGAACATATCA--CCATACAT--TCTCAGAAG 718
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 LysGlyThrGlyValProValGlnLysGlyThrLeuGlnCysGluAlaSerAlaVal 248
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 719 TTAGGGCCGGTGTCCCGTGGGGGAGAGGGGCT--CTGAGTGTGAGCTT---CGAGTGC 774
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ProSerAlaGlu 252
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 775 CCITCGCGGAT 786
  
```

Search completed: September 11, 2003, 05:12:23
 JOE time : 2518 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 03:02:48 ; Search time 39 seconds
(without alignments)
848:257 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMNSISWAIFGL.....RRAGCVLLPLLVLLHLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	1639.5	90.8	344	I56551	neurotrophin - rat
2	1285.5	71.2	338	JC1238	opioid-binding protein
3	1268	70.2	345	JG4025	opioid-binding protein
4	1266	70.1	345	S03199	opioid-binding protein
5	1259	69.7	345	JC1239	opioid-binding protein
6	935.5	51.9	338	JG5519	50k glycoprotein p
7	931.5	51.6	338	JG4776	limbic-system-asso
8	297.5	16.5	333	A31923	amalgam protein pr
9	283.5	15.7	725	IJMSNG	neural cell adhesi
10	283.5	15.7	725	IJMSNL	neural cell adhesi
11	279.5	15.5	725	JEC099	neural cell adhesi
12	279.5	15.5	1091	IJCHNL	neural cell adhesi
13	278.5	15.4	4162	T42633	neural cell adhesi
14	277.5	15.4	858	IJRTNC	connectin/titin -
15	277.5	15.4	1088	IJXLNL	neural cell adhesi
16	276	15.3	761	IJHUNG	neural cell adhesi
17	275.5	15.3	853	IJBONC	neural cell adhesi
18	273.5	15.1	725	JF0100	neural cell adhesi
19	272.5	15.0	1323	PN0568	connectin 3B chli
20	270.5	15.0	1092	JN0635	neural cell adhesi
21	261.5	14.5	1091	S01998	contactin precurs
22	259	14.3	7962	I38346	contactin precurs
23	254.5	14.1	5175	I20952	elastic titin - hu
24	249.5	13.8	1040	T43290	hypothetical prote
25	249.5	13.6	1018	A49356	transient axonal g
26	246.5	13.5	1021	A54744	contactin 1 precu
27	243.5	13.5	1021	A57112	contactin precurs
28	243.5	13.5	1036	S22393	axonin 1 precursor
29	241.5	13.4	1018	JC4211	neural adhesion pr

30	241.5	13.4	1020	2	S05944	neural cell surf
31	240	13.3	3707	2	S18252	heparan sulfate pr
32	235	13.0	662	2	T16525	hypothetical prote
33	234.5	13.0	1040	2	A34695	axonal glycoprotei
34	232.5	12.9	2783	2	T34416	hypothetical prote
35	230.5	12.8	868	2	A46512	CD22 homolog/B lym
36	227.5	12.6	1051	2	A39712	kinase-like protei
37	226	12.5	6642	2	T29757	protein UNC-89 - C
38	225	12.5	4391	2	A38096	perlecan precursor
39	221.5	12.3	862	2	I49583	differentiation an
40	221	12.2	1896	2	T08851	Down Syndrome cell
41	220.5	12.2	898	2	A40114	fasciclin II precu
42	219	12.1	1091	2	A58532	glial cell membran
43	218.5	12.1	1612	2	T30805	cutti protein - mo
44	215.5	11.9	1239	1	A32579	neuroglian - fruit
45	214.5	11.9	1070	2	JC4593	protein-tyrosine k

ALIGNMENTS

RESULT 1

I56551
neurotrophin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: I56551
R:Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J
J. Neurosci. 15, 2141-2156, 1995
A:Title: Cloning of neurotrophin defines a new subfamily of differentially expressed n
A:Reference number: I56551; MUID:95198094; PMID:7891157
A:Accession: I56551
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-344 <RES>
A:Cross-references: EMBL:U16845; NID:g755184; PIDN:AA67445.1; PID:g755185
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter

Query Match 90.8%; Score 1639.5; DB 2: Length 344;
Best Local Similarity 92.9%; Pred No. 1.4e-113;
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY	12	ISWAIFGLAALCLF---	QGVPRSGDATTFFPKAMDNVTVRQGESATLRC	TIDNRTVRVAV	68
DB	9	LPWKLVVSLRLFLVPTGVPVRSGDATTFFPKAMDNVTVRQGESATLRC	TIDNRTVRVAV	68	
QY	69	LNRSTILYAGNDKWLDPRLVLLSNTQYSIEIQNVYVDEGPTCSVQTDNHPKTSRV	128		
DB	69	LNRSTILYAGNDKWLDPRLVLLSNTQYSIEIQNVYVDEGPTCSVQTDNHPKTSRV	128		
QY	129	HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTVRRHISPKAVGVSEDEYLEI	188		
DB	129	HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTVRRHISPKAVGVSEDEYLEI	188		
QY	189	QGITRQSGDYECASNDVAAPVVRVRYKVTNPPYVISEAKGTGVPVGKQKTFLOCEASAV	248		
DB	189	QGITRQSGDYECASNDVAAPVVRVRYKVTNPPYVISEAKGTGVPVGKQKTFLOCEASAV	248		
QY	249	PSAEFFQYKDKRLLEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKGHTNASI	308		
DB	249	PSAEFFQYKDKRLLEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKGHTNASI	308		
QY	309	MLFGPGAVSEVNGTSRRAGCVLLPLLVLLHLLKF	344		
DB	309	MLFGPGAVSEVNGTSRRAGCVLLPLLVLLHLLKF	344		

RESULT 2

JC1238
opioid-binding protein (Clone DU21) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-May-2000
C:Accession: JC1238

C:Accession: JCI1239
 R:Filipman, D.A.; Lee, N.M.; Loh, H.H.
 G:GenBank; 249-254, 1992
 A:Title: Opioid-binding cell adhesion molecule (OBAM)-related clones from a rat brain cDNA library
 A:Reference number: JCI1238; MUID:92347701; PMID:1339369
 A:Accession: JCI1239
 A:Molecule type: mRNA
 A:Residues: 1-345 <LIP>
 A:Cross-references: GB:M88710; NID:g203247; PIDN:AAA40859.1; PID:g203248; GB:M88711; NID:g203249
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 C:Keywords: transmembrane protein

Query Match 69.7%; Score 1259; DB 2; Length 345;
 Best Local Similarity 71.2%; Pred. No. 1.7e-85;
 Matches 240; Conservative 34; Mismatches 59; Indels 4; Gaps 2;

QY 12 ISWAIFTGLAALCLF--OGVPRSGDGFPPKAMDNVTVROGESATLRCTIDNRVTRVAM 68
 DB 9 LPWKLVVYSLRLLFLVPTGVPVRSDDGFPPKAMDNVTVROGESATLRCTIDNRVTRVAM 68
 QY 69 LNRSTILYAGNDKCLDRVLLSNTOTQYSEIQNVYDVGPTCSVOTDNHPTSRV 128
 DB 69 LNRSTILYAGNDKSIDRVLIVNTPTQYSEIQNVYDVGPTCSVOTDNHPTSRV 128
 QY 129 HLIVQSPKIVEISSDINSNGNLSITCIATGRPEPTVTVRHHISPK-AVGFVSEDEYLE 187
 DB 129 HLIVQSPKIVEISSDINSNGNLSITCIATGRPEPTVTVRHHISPK-AVGFVSEDEYLE 187
 QY 188 IQGITREQSGDYEGSASNDVAAPVRRVKVTVNYPYISAKGTGVPVKGKGTLOCEASA 247
 DB 188 IQGITREQSGDYEGSASNDVAAPVRRVKVTVNYPYISAKGTGVPVKGKGTLOCEASA 247
 QY 248 VPSAEQWTKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYNTCVASNKLGHTNAS 307
 DB 248 VPSAEQWTKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYNTCVASNKLGHTNAS 307
 QY 308 IMLFPGAVSEVSGTSSRRAGCVMLPLLVLLHLKLF 344
 DB 308 IMLFPGAVSEVSGTSSRRAGCVMLPLLVLLHLKLF 344
 QY 309 ITLYGPGAVIDGVNSAGRALACLWLSGTFFFAHFFIKF 345
 DB 309 ITLYGPGAVIDGVNSAGRALACLWLSGTFFFAHFFIKF 345

RESULT 6

JC5519
 50K glycoprotein precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Nov-2000
 C:Accession: JC5519
 R:Hancock, K.A.; Gooley, A.A.; Jeffrey, P.L.
 A:Title: AVGP50, a predominantly axonally expressed glycoprotein, is a member of the Igl
 A:Reference number: JC5519; MUID:97225999; PMID:9073169
 A:Accession: JC5519
 A:Molecule type: mRNA
 A:Residues: 1-338 <HAN>
 A:Experimental source: brain
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 C:Keywords: glycoprotein
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-338/Product: 50K glycoprotein #status predicted <MAT>
 F:46-113/Domain: immunoglobulin homology <IMM1>
 F:146-199/Domain: immunoglobulin homology <IMM2>
 F:232-292/Domain: immunoglobulin homology <IMM3>
 F:40,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 51.0%; Score 936.5; DB 2; Length 338;
 Best Local Similarity 56.0%; Pred. No. 1e-61;
 Matches 192; Conservative 55; Mismatches 83; Indels 5; Gaps 4;

QY 20 LAALCLF-OGVPRSGDGFPPKAMDNVTVROGESATLRCTIDNRVTRVAMNRSTILYAG 78
 DB 17 LRLCLLPTGLPVRSD--FTRGTDNITVRQDGTALRCFVDESKVAMLRNSGIIFAG 74

QY 79 NDKWCLDRPVLLSNTOTQYSEIQNVYDVGPTCSVOTDNHPTSRVHLIVQVSPKI 138
 DB 75 EDKWSLDPRVELEKSRPLEYSLRIOKVDVYDEGTYCSVQTOHHPKTSQVYLLIVQVPPKI 134
 QY 139 VEISSDISINEGNNLSITCIATGRPEPTVTVRHHISPKAVGFVSEDEYLEIQTREOSGD 198
 DB 135 SNISSDITVNEGSNTVLCMANGRPETVTVRHLIPTGKEFEGBEEYLEILGITRQSGK 194
 QY 199 YECASNDVAAPVRRVKVTVNYPYISAKGTGVPVKGKGTLOCEASAVPSAEFQWYKD 258
 DB 195 YECASNDVAAPVRRVKVTVNYPYISAKGTGVPVKGKGTLOCEASAVPSAEFQWYKD 254
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYNTCVASNKLGHTNASIMLFGPGAVSE 318
 DB 255 DTR-INSANGLEIKSTGSSQLLVANVTEEHYNTCVAAANKLGVNLSLYLRPG-TGR 312
 QY 319 VSGTSSRRAGCVMLPLLVLLHLK 343
 DB 313 VDNQSVSLAVPLMLLAASLLCLLSK 337

RESULT 7

JC4776
 Lmbic-system-associated membrane protein precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000
 C:Accession: JC4776
 R:Pimenta, A.F.; Fischer, I.; Levitt, P.
 A:Title: cDNA cloning and structural analysis of the human limbic-system-associated m
 A:Reference number: JC4776; MUID:96235133; PMID:8666243
 A:Accession: JC4776
 A:Molecule type: mRNA
 A:Residues: 1-338 <PIN>
 A:Cross-references: GB:U1901; NID:g1276898; PIDN:AAC50569.1; PID:g1276899
 A:Experimental source: brain
 C:Comment: This is a neuronal surface glycoprotein distributed in cortical and subcon
 C:Genetics:
 A:Gene: lamp
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter
 C:Keywords: brain; glycoprotein; membrane protein; phosphoprotein
 F:1-7/Domain: signal sequence #status predicted <SIG>
 F:333-338/Region: hydrophobic
 F:40,66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status p
 F:42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predict
 F:195,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 51.6%; Score 931.5; DB 2; Length 338;
 Best Local Similarity 55.4%; Pred. No. 2.4e-61;
 Matches 180; Conservative 60; Mismatches 80; Indels 5; Gaps 4;

QY 20 LAALCLF-OGVPRSGDGFPPKAMDNVTVROGESATLRCTIDNRVTRVAMNRSTILYAG 78
 DB 17 LRLCLLPTGLPVRSD--FTRGTDNITVRQDGTALRCFVDESKVAMLRNSGIIFAG 74
 QY 79 NDKWCLDRPVLLSNTOTQYSEIQNVYDVGPTCSVOTDNHPTSRVHLIVQVSPKI 138
 DB 75 HDKWSLDPRVELEKSRPLEYSLRIOKVDVYDEGTYCSVQTOHHPKTSQVYLLIVQVPPKI 134
 QY 139 VEISSDISINEGNNLSITCIATGRPEPTVTVRHHISPKAVGFVSEDEYLEIQTREOSGD 198
 DB 135 SNISSDITVNEGSNTVLCMANGRPETVTVRHLIPTGKEFEGBEEYLEILGITRQSGK 194
 QY 199 YECASNDVAAPVRRVKVTVNYPYISAKGTGVPVKGKGTLOCEASAVPSAEFQWYKD 258
 DB 195 YECASNDVAAPVRRVKVTVNYPYISAKGTGVPVKGKGTLOCEASAVPSAEFQWYKD 254
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYNTCVASNKLGHTNASIMLFGPGAVSE 318
 DB 255 DTR-INSANGLEIKSTGSSQLLVANVTEEHYNTCVAAANKLGVNLSLYLRPG-TGR 312
 QY 319 VSGTSSRRAGCVMLPLLVLLHLK 343
 DB 313 VDNQSVSLAVPLMLLAASLLCLLSK 337

Db 314 I-NGSISLAVPLWLLAASLLCLLSK 337

RESULT 8
A31923
analgam protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
R:Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 35, 589-600, 1988
A:Title: Characterization of amalgam: a member of the immunoglobulin superfamily from D.
A:Reference number: A31923; MUID:89028670; PMID:3141062
A:Accession: A31923
A:Molecule type: DNA
A:Residues: 1-333 <SEE>
A:Cross-references: GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921
A:Gene: FlyBase:Ana
A:Cross-references: FlyBase:FBgn0000071

Query Match 16.5%; Score 297.5; DB 2: Length 333;
Best Local Similarity 29.7%; Pred. No. 1.4e-14;
Matches 87; Conservative 43; Mismatches 136; Indels 27; Gaps 11;

QY 44 NVTVROGESATLRCTIDN-RVTRVAVLNR-----STILVAGNDKWCPLDP--VVLLSN 93
DB 33 DVASVGDSEVENCIVEVQGLSVSAKRPESDTNSVLSNRNLSLPDKRYNVTVTEG 92
QY 94 TQTQ---YSIEIQNDVDEGPTCYQTDNHPK-TSRVHLIVQVSPKIVE-ISSDISIN 148
DB 93 PKTGSALTYFRIONIEVSDMGPIECQVLVSATEKVKLSLQIKTPPVIAENPKSTLVT 152
QY 149 EGNISITCIATGRPEPTVWRH-----ISPKAVGVFSEDEYLEIQTREOSGDYECSSAS 204
DB 153 EQGLEUTCHANGFKPTISWAREHNAVMP-AGGHLAEPTRLIRSVHRMDRGVYICIAQ 211
QY 205 NDVAAPVVRVRYVNYPPYIS-EAKGTGVPVQKGTQLOCEASAVPSAEFOWYKDKRLI 263
DB 212 NGEQOPDKLIRVEFRPQIAVQRPKIAQVSHSAECSVQGYPAFTVVMKNGVPL- 270
QY 254 EGKKGKVENR-----PFLSKLIFFNVSEHDYGNVTCVASNKLIGHTNASIMLF 311
DB 27: QSSRHEVANTASSGTTTSLVRIDSVGEEDFGDYCNATNKLGHADARLHLF 323

RESULT 9
IJMSNL
neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse
N:Alternate names: NCAM-120
C:Species: Mus musculus. (house mouse)
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
R:Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A:Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A:Reference number: A29673; MUID:87246524; PMID:3595563
A:Accession: A29673
A:Molecule type: mRNA
A:Residues: 1-725 <BAR>
A:Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R:Barthes, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A:Title: Differential splicing and alternative polyadenylation generates distinct NCAM t
A:Reference number: S00382; MUID:88283628; PMID:3396334
A:Accession: S00382
A:Molecule type: DNA
A:Residues: 542-656, D', 658-725 <BA2>
A:Cross-references: EMBL:X07195
R:Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A:Title: Structural and immunological characterization of the amino-terminal domain of
A:Reference number: A44290; MUID:86140120; PMID:3512556

A:Accession: A44290
A:Molecule type: protein
A:Residues: 20-36 <ROU>
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM
C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:1
C:Genetics:
A:Gene: NCAM
A:Map position: 9
A:Introns: 701/1
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; i
C:Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membra
F:1-19/Domain: signal sequence status predicted <SIG>
F:14-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-290/Domain: immunoglobulin homology <IMM3>
F:263-272/Region: NCAM binding #status predicted
F:323-388/Domain: immunoglobulin homology <IMM4>
F:420-482/Domain: immunoglobulin homology <IMM5>
F:519-596/Domain: fibronectin type III repeat homology <FN3A>
F:625-685/Domain: fibronectin type III repeat homology <FN3B>
F:41-96.139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F:222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 15.7%; Score 283.5; DB 1: Length 725;
Best Local Similarity 25.8%; Pred. No. 4.1e-13;
Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

QY 44 NVTVROGESATLRCTIDN-RVTRVAVLNRSTILVAGNDKWCPLDPV-----LLSNQ 95
DB 222 NAFNLGQSVILVCDAG-----PPEPTM-----SWTKGEPIENEEDERSRVS 268
QY 96 TQYSIEIQNDVDEGPTCYQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNISL 155
DB 269 DSSEVTRIRNVKNDSEAVYCAENKAGEQDASHLKVFAPKTYVYENQTAEMESEQVL 328
QY 156 TCATGRPEPTVWR-----HISPKAVGVFSEDEYLEIQTREQSGDYE 200
DB 329 TCASGDDPSTITWTRTSTRNTSSSEEDLDGHVVRSHARVSS---LTKSIQVRDAGEYM 385
QY 201 CSASNDVAAPVVRVRYVNYPPYIS-EAKGTGVPVQKGTQLOCEASAVPSAEFOWYKDK 260
DB 386 CTASNTIGDQ-SQSIDLEFYAPKLOGFVAVYTWEGNQVNIITCEVFAYPSATISWFRDQ 444
QY 261 RLIEGK-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLIGHTNASIML 310
DB 445 LLPSSNYSNIIKYNTSPASYLEVTPDSEDFGNVCTAVNRIGQESLEFIL 495

RESULT 10
IJMSNL
neural cell adhesion molecule-1 precursor, long domain splice form - mouse
N:Alternate names: NCAM-180
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C:Accession: A29673; S00384; A28281; A44290; S00383
R:Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fon
EMBO J. 6, 907-914, 1987
A:Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,
A:Reference number: A29673; MUID:87246524; PMID:3595563
A:Accession: A29673
A:Molecule type: mRNA
A:Residues: 1-548, T', 550-571, T', 573-574, D', 576-588, MQPS', 593, S', 595-599, P', 601,
A:Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R:Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.
Nucleic Acids Res 15, 8621-8641, 1987
A:Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse n
A:Reference number: S00844; MUID:88067687; PMID:3684567
A:Accession: S00844
A:Molecule type: mRNA
A:Residues: 529-809,1077-1115 <SAN>

A:Cross-references: EMBL:X06328; NID:G53322; PIDN:CAA29641.1; PID:g817984
R:Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A:Title: Differential splicing and alternative polyadenylation generates distinct NCAM
A:Reference number: S00382; MUID:88283628; PMID:3396534
A:Accession: S00384
A:Molecule type: DNA
A:Residues: 642-1115 <BA3>
A:Cross-references: EMBL:X07195
R:Barthelemy, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A:Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
A:Reference number: A28281; MUID:88247737; PMID:2454455
A:Accession: A28281
A:Molecule type: mRNA
A:Residues: 804-1081 <BA3>
A:Cross-references: EMBL:X07244; NID:G53321; PIDN:CAA30230.1; PID:g929720
R:Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A:Title: Structural and immunological characterization of the amino-terminal domain of
A:Reference number: A44290; MUID:86140120; PMID:3512556
A:Accession: A44290
A:Molecule type: protein
A:Residues: 20-36 <ROU>
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C:Comment: Several forms of NCAM are produced by alternative splicing. See also, PIR:J0MS
C:Genetics:
A:Gene: NCAM
A:Map position: 9
A:Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-809/1077-1115/Product: neural cell adhesion molecule, long domain splice form #status experi
F:20-711/Domain: extracellular #status predicted <EXT>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-290/Domain: immunoglobulin homology <IMM3>
F:262-272/Region: NCAM binding #status predicted
F:323-388/Domain: immunoglobulin homology <IMM4>
F:420-482/Domain: immunoglobulin homology <IMM5>
F:519-596/Domain: fibronectin type III repeat homology <FN3A>
F:525-685/Domain: fibronectin type III repeat homology <FN3B>
F:712-729/Domain: transmembrane #status predicted <IMM>
F:1196-139-189-235-286-330-386-427-480/disulfide bonds: #status predicted
F:222-515-348-424-450-479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 283.5; DB 1; Length 1115;
Best Local Similarity 25.8%; Pred. No. 7.1e-13;
Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

QY 44 NTVROGESATLRCTIDNRVTRVAVLNRSTILYAGNDKWCIDPRV-----LLSNQ 95
Db 222 NATANLQSVTLVCDAG-----FPEPTM-----SWTKDGEPIENEEDERSRVS 268

QY 96 TQISEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVSEISDLSINEGNISL 155
Db 269 DSSEVIRNVDRNDKDAEIVCIAENKAGEQDASHLKVPKPKITYVFNQVAMELEQVTL 328

QY 156 TCTATGRPEPTVTR-----HISPKAVGVSEDEYLEIOGTITREQSGDYE 200
Db 329 TCASAGDPIPSITWTRTSTRNTISSEEDLDGDMVVRSHARVSS---LTLKIQIRDAGETM 385

QY 201 CSASNDVAAPVRRKVVNPPYPISEAKGTGVPVCGKGTQCEASAVPSAEQWYKDDK 260
Db 386 CTASNTIGDQ-SQSIDLFEQAPKLPQVAVTWEGNVNITCEVAFPSATISWFRDQ 444

QY 261 RLTEGR-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNLGHTNASIML 310

Db 445 LLPSSNYSNIIKYNTPSASYLEVTPDSEDFGNVNTAVNRIGQESLEFIL 495

RESULT 11

QY 0099

Neural cell adhesion molecule 1 - African clawed frog

N:Alternate names: NCAM 1

C:Species: Xenopus laevis (African clawed frog)

C>Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: JE0099

R:Kudo, M.; Takayama, E.; Takakuma, T.; Shiohawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A:Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMS) as the

A:Reference number: JE0099; MUID:98204770; PMID:9535795

A:Accession: JE0099

A:Molecule type: mRNA

A:Residues: 1-725 <KUD>

A:Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g3116227

A:Experimental source: heart

C:Comment: This protein mediates and regulates various cell-cell interactions through

C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; i

F:413-475/Domain: immunoglobulin homology <IMM>

F:512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 15.5%; Score 279.5; DB 2; Length 725;
Best Local Similarity 27.9%; Pred. No. 8.1e-13;
Matches 80; Conservative 50; Mismatches 120; Indels 37; Gaps 11;

QY 44 NTVROGESATLRCTIDNRVTRVAVLNRSTILYAGNDKWCIDPRVLLSNQTSYIEI 102

Db 219 NATAKAESVILSCDAGFPDPEISLWKKGEPIEDGEER-----ISFEDQSEMTI 269

QY 103 QNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVSEISDLSINEGNISLTCIATGR 162

Db 270 HHVEKDEAEYSIANNQAGEATILKVVAKPKITYVENKTAV-ELDEITLTCEASGD 328

QY 163 PEPTVTV-----RHISPKAV-----GFVSEDEYLEIOGTITRE-----OSGDYECASNDVAAP 210

Db 329 PIPSITWTRVARNISSEATLDGHIIVKHEIRMSALTLDIOYTDAGEYFCIASNPFGVD 398

QY 211 VVRKVVNPPYPISEAKGTGVPV-----GQKGTQCEASAVPSAEQWYKDDKRLIE 264

Db 389 -MQMVFQVYAPK-----RG---PVVYTWEGNVNITCEVAFHRAAVTWFRDQQLPS 441

QY 265 GK-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNLGHTNASIML 310

Db 442 SNFSNIIKYSVGTSSSLEVPDSEDFGNVNTAVNRIGQESLEFIL 488

RESULT 12

IJCNNL

neural cell adhesion molecule long domain form precursor - chicken

N:Alternate names: NCAM-180

N:Contains: neural cell adhesion molecule, short domain form (NCAM-140)

C:Species: Gallus gallus (chicken)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

R:Cunningham, B.A.; Hemperly, J.J.; Murray, B.A.; Prediger, E.A.; Brackenbury, R.; Ed

Science 236, 799-806, 1987

A:Title: Neural cell adhesion molecule: structure, immunoglobulin-like domains, cell

A:Reference number: A43613; MUID:87206190; PMID:3576199

A:Accession: A43613

A:Molecule type: mRNA

A:Residues: 1-175 <CU2>

A:Cross-references: GB:M15860

A:Accession: B43613

A:Molecule type: protein

A:Residues: 20-44; 120-127; 202-221; 320-342; 399-415; 640-659; 822-828 <CUN>

A>Note: Asn-222 probably binds carbohydrate; Asn-226 probably does not

R:Hemperly, J.J.; Murray, B.A.; Edelman, G.M.; Cunningham, B.A.

Proc. Natl. Acad. Sci. U.S.A. 83, 3037-3041, 1986

A:Title: Sequence of a cDNA clone encoding the polystyalle acid-rich and cytoplasmic d

A:Reference number: A25435; MUID:86206089; PMID:34584261

A:Accession: 500846
 A:Molecule type: mRNA
 A:Residues: 1-858 <SMA>
 A:Cross-references: EMBL:X06564
 R:Small, S.J.; Akesson, R.
 J. Cell Biol. 111, 2089-2096, 1990
 A:Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
 A:Reference number: A37795; MUID:91035620; PMID:1699951
 A:Accession: 937795
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 340-381 <SM2>
 R:Small, S.J.; Haines, S.L.; Akesson, R.A.
 Neuron 1, 1007-1017, 1988
 A:Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
 A:Reference number: 158136; MUID:90166485; PMID:2483093
 A:Accession: 158136
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 355-364 <RES>
 A:Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
 A:Title: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
 C:Comment: Various forms of NCAM are produced by alternative splicing.
 C:Genetics:
 A:Gene: NCAM
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-858/Product: neural cell adhesion molecule, short domain form #status predicted <M
 F:20-721/Domain: extracellular #status predicted <EXT>
 F:34-98/Domain: immunoglobulin homology <IMM1>
 F:132-132/Domain: immunoglobulin homology <IMM2>
 F:132-132/Region: heparin binding #status predicted
 F:151-156/Region: heparin binding #status predicted
 F:228-230/Domain: immunoglobulin homology <IMM3>
 F:263-272/Region: NCAM binding #status predicted
 F:323-398/Domain: immunoglobulin homology <IMM4>
 F:430-432/Domain: immunoglobulin homology <IMM5>
 F:529-606/Domain: fibronectin type III repeat homology <FN3A>
 F:535-695/Domain: fibronectin type III repeat homology <FN3B>
 F:722-739/Domain: transmembrane #status predicted <TM>
 F:740-858/Domain: intracellular #status predicted <INT>
 F:741-95,139,235,330,396,437-490/Disulfide bonds: #status predicted
 F:222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.4%; Score 277.5; DB 1; Length 858;
 Best Local Similarity 25.5%; Pred. No. 1.4e-12;
 Matches 75; Conservative 50; Mismatches 132; Indels 37; Gaps 7;
 QY 44 NVTVROGESATLRCTIDN-RVTVAVMLNRSTILYAGNDKWCCLDPRVLLSNTQTSIEI 102
 DB 222 NATANLGOSVILVCDADGFPPTMSHTKGEPIENEE-----DDEKHFSDSSE--LTI 275
 QY 103 QNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGR 162
 DB 276 RNVKNDKAEYCYTAENKAGEQDASHLKVFAPKITTVENQTALELEQVILTCEASGD 335
 QY 163 PEPTVTR-----HISPRAGVFSEDEYLEIQITREQSG 197
 DB 336 PIPSITWRTSTNISSEKASWTRPEKQETLDGHHVVRSHARVSS---LTLKSIQYTDAG 392
 QY 198 DYCSASNDVAAPVVRVVKVTVNPPYISEAKGTGVPVGGKTLQCEASAVPSAEFOYK 257
 DB 393 EYICATSNIGOD-SQSMYLEVOYAPKLOGPVAVTVWEGNVNITCEVAFPSATISWFR 451
 QY 258 DKKRLIEG-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKLGHFNASIML 310
 DB 452 DQGLPSSNYSNIKINPSSASTLEVTPDSEDFGNCTAVNRIGESLEFIL 505

RESULT 15
 IJXLNL

neural cell adhesion molecule long domain form precursor - African clawed frog

N:Alternate names: NCAM-180
 N:Contains: neural cell adhesion molecule, short domain form (NCAM-140).
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
 C:Accession: 509600
 R:Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
 Nucleic Acids Res. 17, 10321-10335, 1989
 A:Title: Primary structure and developmental expression of a large cytoplasmic domain
 A:Reference number: 509600; MUID:90098871; PMID:2481269
 A:Accession: 509600
 A:Molecule type: mRNA
 A:Residues: 1-1088 <KRI>
 A:Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610
 A:Note: the authors translated the codon AAA for residue 970 as Leu
 C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM
 C:Comment: Several forms of NCAM are produced by alternative splicing.
 C:Genetics:
 A:Gene: NCAM
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; i
 C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding;
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-1088/Product: neural cell adhesion molecule, long domain form #status predicted
 F:20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status
 F:20-705/Domain: extracellular #status predicted <EXT>
 F:34-95/Domain: immunoglobulin homology <IMM1>
 F:129-188/Domain: immunoglobulin homology <IMM2>
 F:149-153/Region: heparin binding #status predicted
 F:158-182/Region: heparin binding #status predicted
 F:225-284/Domain: immunoglobulin homology <IMM3>
 F:317-381/Domain: immunoglobulin homology <IMM4>
 F:413-475/Domain: immunoglobulin homology <IMM5>
 F:512-589/Domain: fibronectin type III repeat homology <FN3A>
 F:618-679/Domain: fibronectin type III repeat homology <FN3B>
 F:706-723/Domain: transmembrane #status predicted <TM>
 F:724-1088/Domain: intracellular #status predicted <INT>
 F:41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
 F:219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 15.4%; Score 277.5; DB 1; Length 1088;
 Best Local Similarity 27.9%; Pred. No. 1.9e-12;
 Matches 80; Conservative 49; Mismatches 121; Indels 37; Gaps 11;
 QY 44 NVTVROGESATLRCTIDN-RVTVAVMLNRSTILYAGNDKWCCLDPRVLLSNTQTSIEI 102
 DB 219 NATANMAESVYLSCADGFPDPEISLKKGEPIEDGEK-----ISFNDSQSEMTI 269
 QY 103 QNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGR 162
 DB 270 HHVERKDDAEVSCANNQAGEAETILKYAKPITTVENKTV-ELDEITLTCESGD 328
 QY 163 PEPTVTR-----RHISPRAV---GFVSEDEYLEIQITRE-----OSGDYCSASNDVAAP 210
 DB 329 PIPSITWRTAVNRNISESATTLDGHHVVRSHARVSS---LTLKSIQYTDAGEYFCIASNPIGVD 388
 QY 211 VVRVVKVTVNPPYISEAKGTGVPV-----GOKGTLOCEASAVPSAEFOYKDKRLIE 264
 DB 389 -MOAMYFEVQAPKI---RG---PVVYVTEGPNVITCEVFAHPRAAVTWFRDQGLPSS 441
 QY 265 GK-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKNKLGHFNASIML 310
 DB 442 SNFSNIKISGPTSSSLEVPDSEDFGNCTAVNRIGESLEFIL 488

Search completed: September 11, 2003, 03:05:44
 Job time: 40 secs